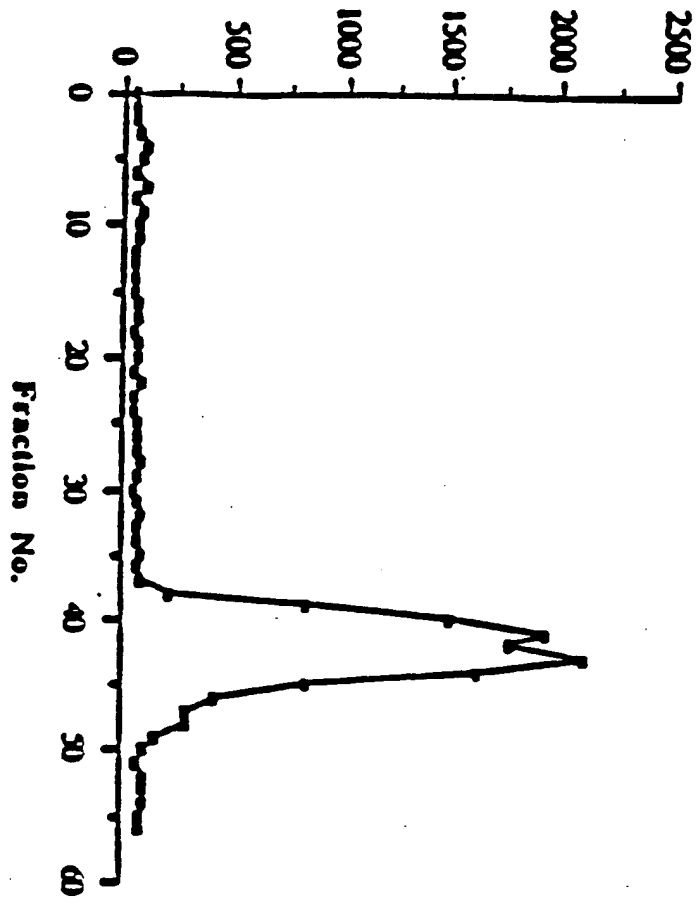


FIGURE 1

08736019-102296



COUNTS 1-125



Hydroxylapatite HPLC

FIGURE 2

08736019-102296

Counts 1-125

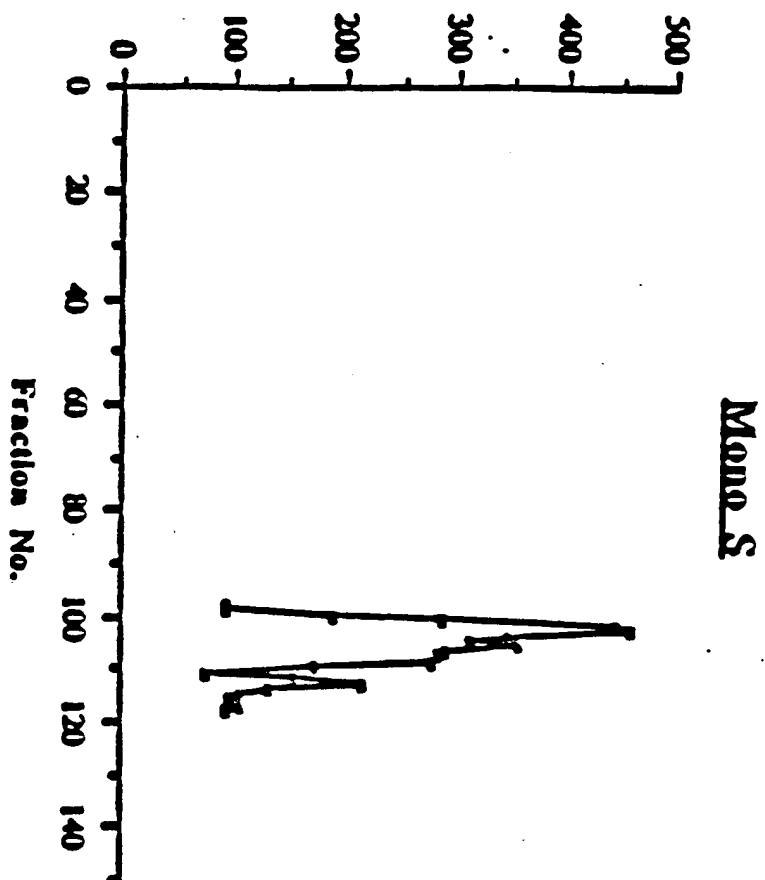


FIGURE 3

08736019-102296

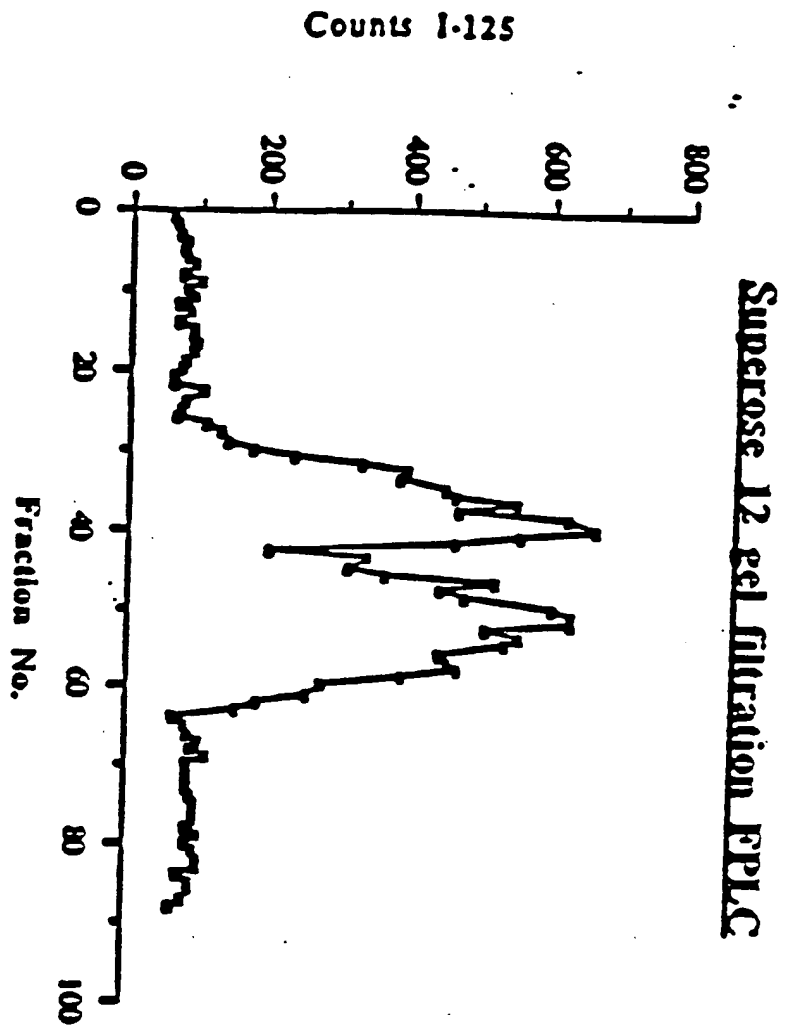


FIGURE 4

08736019-102296

Reversed phase HPLC

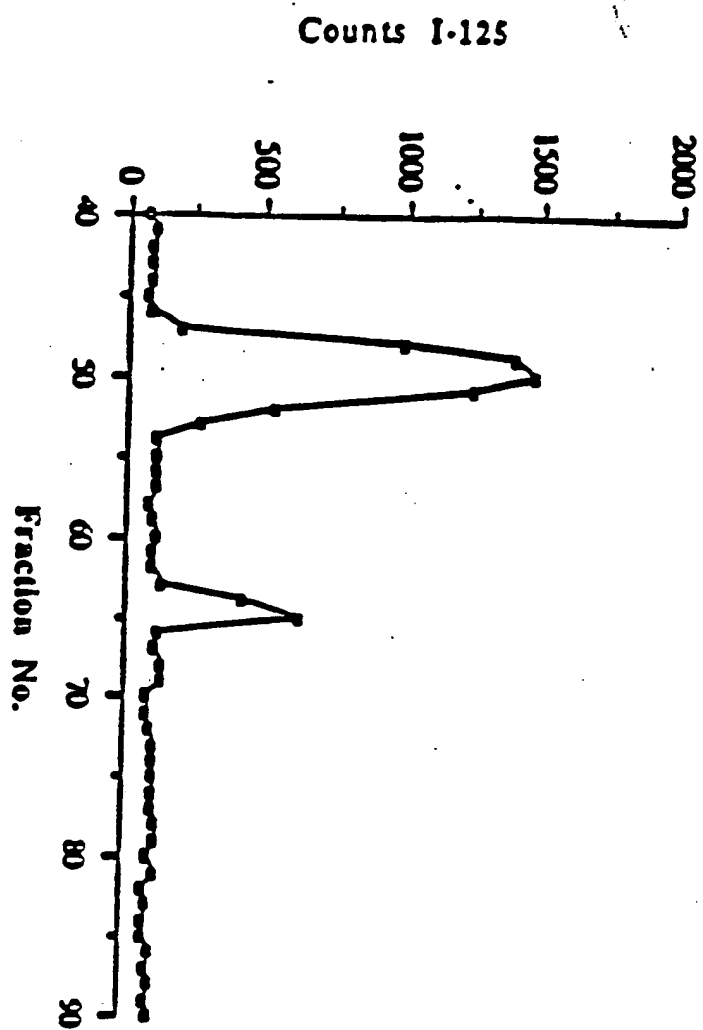


FIGURE 5

00736019-102296

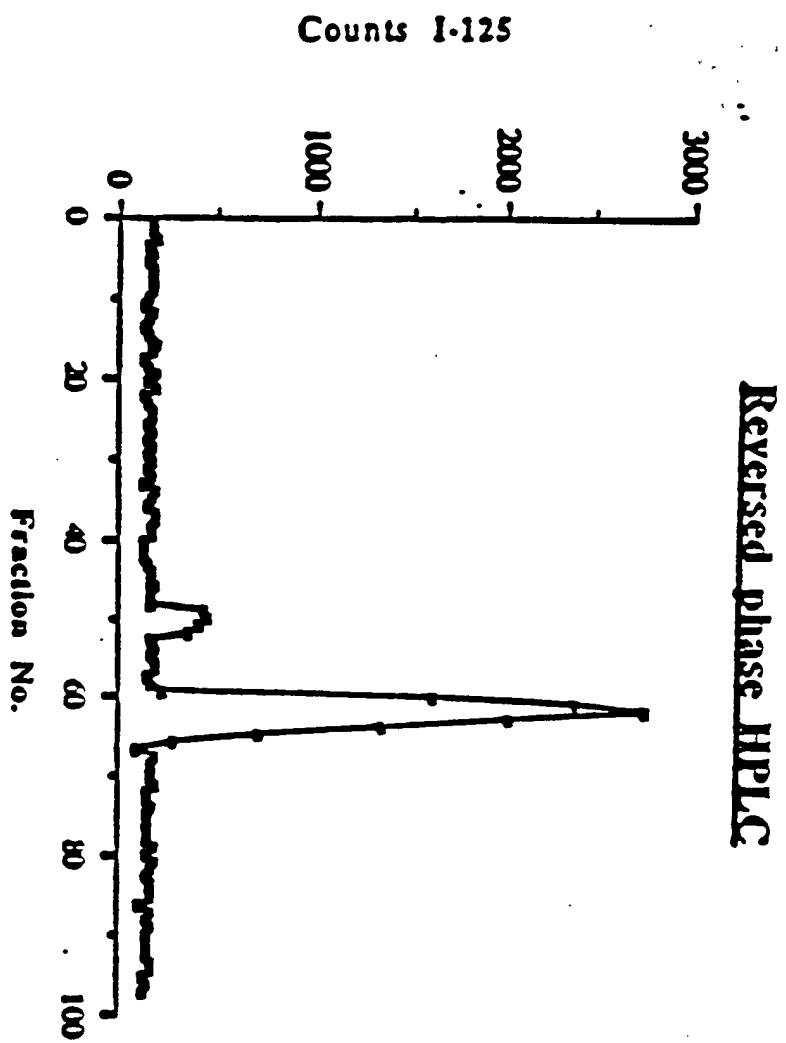


FIGURE 6

002736019-102296

Counts 1-125

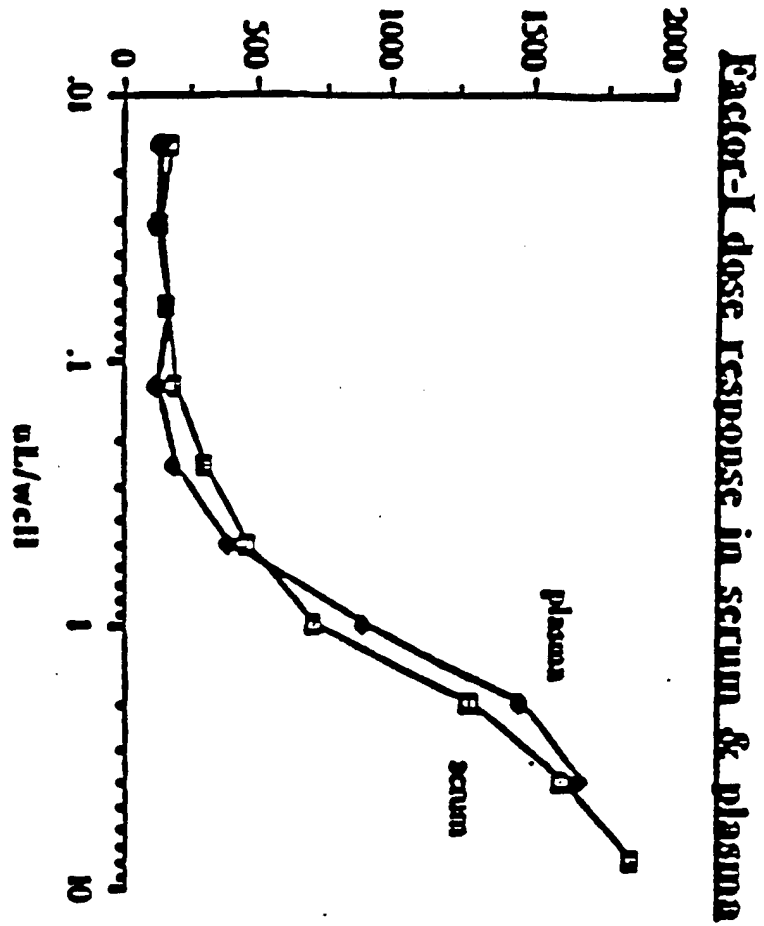


FIGURE 7

08736019-102296

Factor-II dose response in serum or plasma

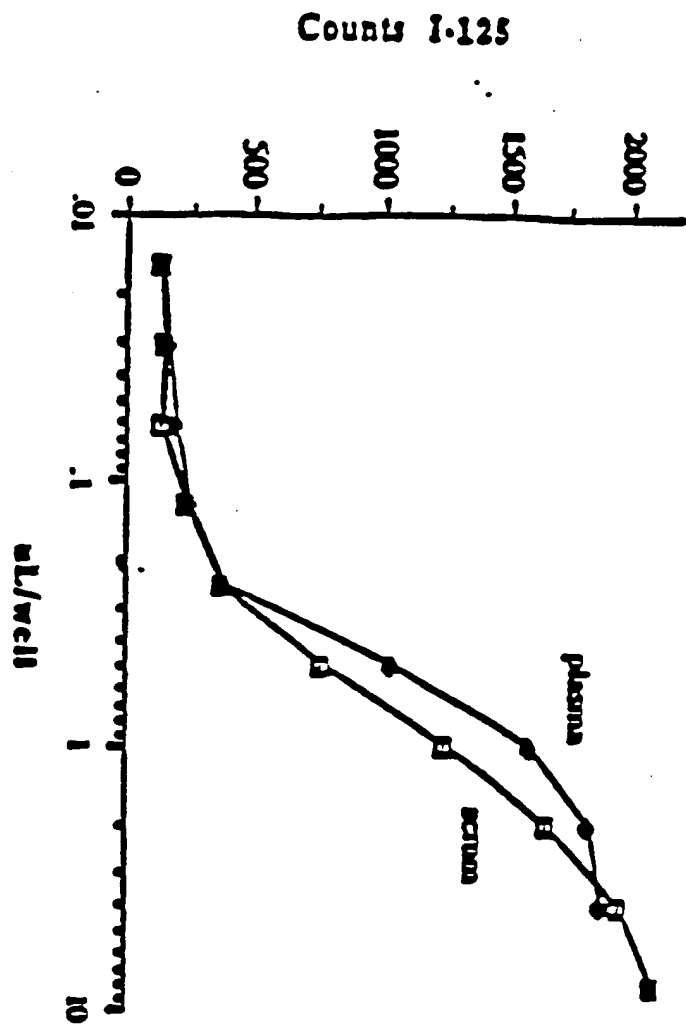


FIGURE 8

FIGURE 9

IF-1 01

Normidine
F K G D A H T E (seq ID no: 1)

IF-1 02

Tryptophan
K M A S L A D E Y E Y M X K . (seq ID no: 2)

IF-1 03

K M T E T S S G L X L K . (seq ID no: 3)

IF-1 04

K M K L G E M W A E (seq ID no: 4)

IF-1 05

K M L G E K N A (seq ID no: 5)

IF-1 06

K M I K S E H A G L S I G D T A K . (seq ID no: 6)

IF-1 07

K M A S L A D E Y E Y M N K . (seq ID no: 7)

IF-1 08

K M I K G E H P G L S I G D V A K . (seq ID no: 8)

IF-1 09

K M M S E Y A F F V O T X R . (seq ID no: 9)

IF-1 10

K M S E H P G L S I G D T A K . (seq ID no: 10)

IF-1 11

K M A G Y F A E X A R . (seq ID no: 11)

IF-1 12

K M K L E F L X A K . (seq ID no: 12)

IF-1 13

K M T T E M A S E O G A (seq ID no: 13)

IF-1 14

K M A K E A L A A L K . (seq ID no: 14)

IF-1 15

K M F V L O A K K . (seq ID no: 15)

IF-1 16

K M L G E M W (seq ID no: 16)

PMG-1

PMG-1

PMG-17

PMG-2

PMG-1

PMG-2

PMG-1

Protease V8 peptides

E T O P D P G O I L K K V P M V I G A Y T (seq ID no: 169)

E Y K C L K F K W F K K A T V M (seq ID no: 17)

E A K Y F S K X D A (seq ID no: 18)

E X K F Y V P (seq ID no: 19)

E L S F A S V R L P G C P P G V D P M V S F P V A L

Uta-1

Uta-1 (seq ID no: 71)

IF-1 17

IF-1 18

IF-1 19

IF-1 20

IF-1 21

Figure 10

A

OCF-1 01	FRGDANTE	(Seq ID no: 1)
OCF-1 02	ASLADYEYMK	(Seq ID no: 22)
OCF-1 03	TESSSGLXLK	(Seq ID no: 23)
OCF-1 07	ASLADYEYMK	(Seq ID no: 24)
OCF-1 11	AGYFAEXAN	(Seq ID no: 25)
OCF-1 13	TENASEOGA	(Seq ID no: 26)
OCF-1 14	AKELALALK	(Seq ID no: 27)
OCF-1 15	FVLQAKK	(Seq ID no: 28)
OCF-1 17	ETOPDFGQILKKVPNVIGAYT	(Seq ID no: 29)
OCF-1 18	EYKCLKKMFKNATVM	(Seq ID no: 17)

B

OCF-1 20	EXKTYVP	(Seq ID no: 19)
OCF-1 12	KLEFLXAK	(Seq ID no: 32)

Figure 11

GGF-II 01 K/R VHQVWAAK*
GGF-II 02 K/R YIFFMEPEAXSSG
GGF-II 03 K/R LGAWGPPAFPVX.Y
GGF-II 04 K/R WVVVIEGK*
GGF-II 05 K/R ALAAAGYDVEK*
GGF-II 06 K/R LVLR*
GGF-II 07 K/R XXYPGQITSN
GGF-II 08 K/R ASPVSVGSGVQELVQR*
GGF-II 09 K/R VCLLTVAALPPT
GGF-II 10 K/R DLLLXV

Trypsin peptides

(SEQ ID NO: 45)
(SEQ ID NO: 46)
(SEQ ID NO: 47)
(SEQ ID NO: 48)
(SEQ ID NO: 164)
(SEQ ID NO: 165)
(SEQ ID NO: 166)
(SEQ ID NO: 49)
(SEQ ID NO: 50)
(SEQ ID NO: 53)

Histone H1

Trypsin

GF-II 11
GF-II 12

Lysyl Endopeptidase-C peptides

KVHQVWAAK*
KASLADSGEYMXK*

(SEQ ID NO: 51)
(SEQ ID NO: 52)

08736019-10296

Figure 12

A

GGF-II 01	VHQVWAAK	(SEQ ID NO: 45)
GGF-II 02	YIFFMEPEAXSSG	(SEQ ID NO: 46)
GGF-II 03	LGAWGPPAFPVXY	(SEQ ID NO: 47)
GGF-II 04	WFVVIEGK	(SEQ ID NO: 48)
GGF-II 08	ASPVSVGSVQELVQR	(SEQ ID NO: 49)
GGF-II 09	VCLLTVAALPPT	(SEQ ID NO: 50)
GGF-II 11	KVHQVWAAK	(SEQ ID NO: 51)
GGF-II 12	KASLADSGEYMXK	(SEQ ID NO: 52)

B

Novel Factor II Peptides - others

GGF-II 10	DLLLXV	(SEQ ID NO: 53)
-----------	--------	-----------------

08736019-102296

Comparison of BrUdJ JSA and [125 I]UdR counting method for the DNA synthesis assay in Schwann cell cultures

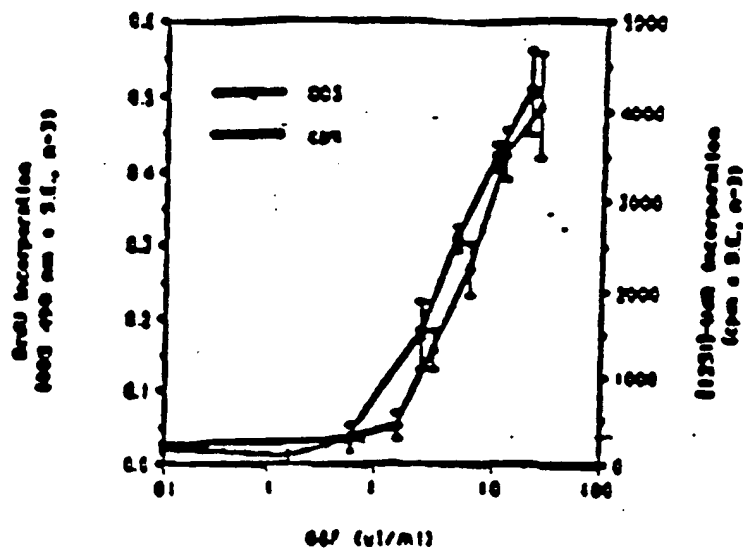


Fig. 13

Comparison of Br-UdR immunoreactivity and Br-UdR labelled cell number

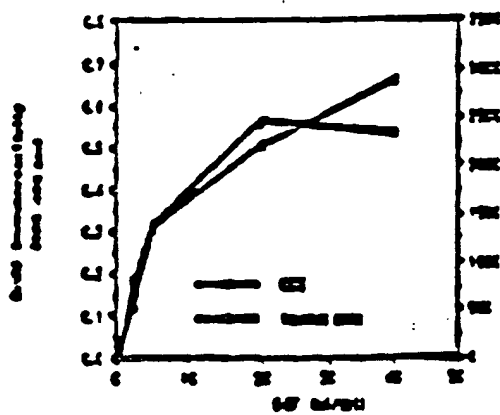


Fig. 14a
4/1/82

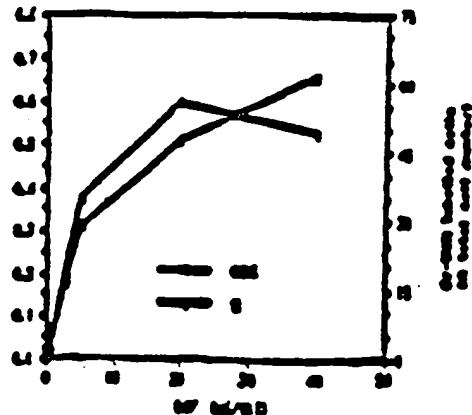


Fig. 14b.

Mitogenic response of rat sciatic nerve Schwann cell to GGFs

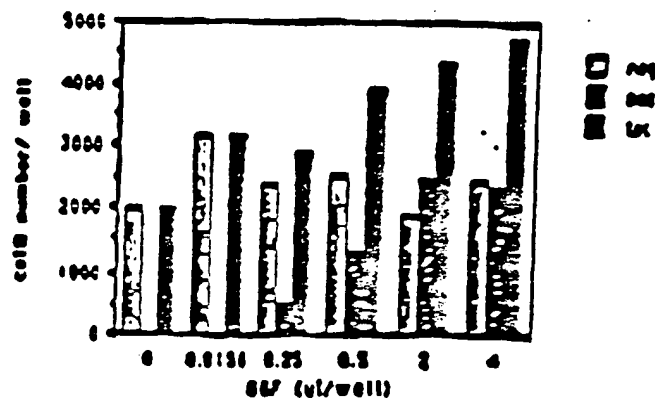


Fig 15

DNA synthesis in rat sciatic nerve Schwann cells and 3T3 fibroblasts in the presence of GGFs

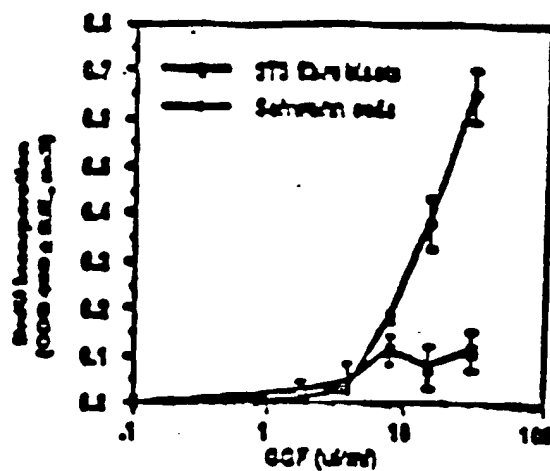


Fig 16.

08736019-102296

Mitogenic response of BHK 21 C13 cells to FCS and GGFs

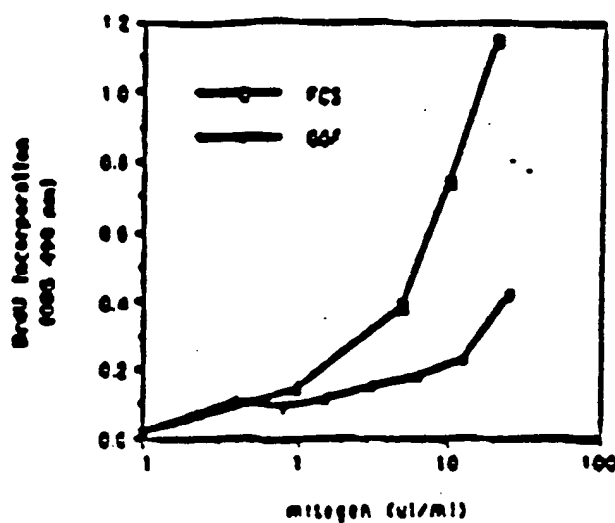


Fig. 17

Survival and proliferation of BHK21 C13 cell microcultures after 48 hours in presence of GGFs

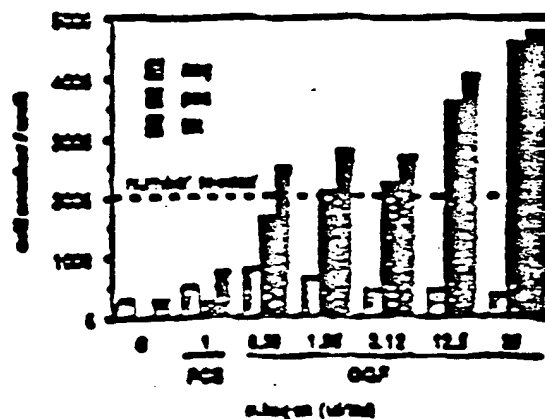


Fig. 18.

Mitogenic response of C6 cells to FCS

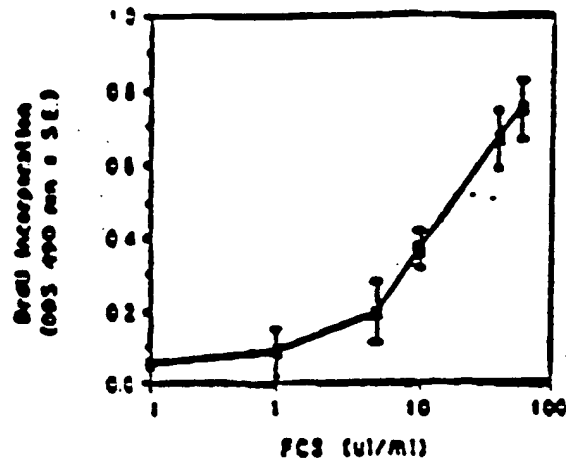


Fig 19.

Mitogenic response of C6 cells to aFGF and GGFs

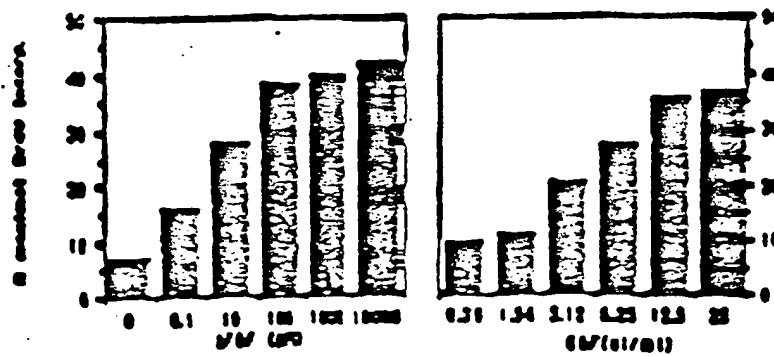


Fig 20

08736019-102296

FIGURE 21

DISCONTINUOUS OLIGONUCLEOTIDE PROBES FOR FACTOR I AND FACTOR II

Oligo	Sequence	Peptide	
535	TTTAAAGCGGAGYGCNCAYAC!	GGFI-1	(SER ID NO: 54)
536	CATRTAYTCTRTAYTCTRTGCG!	GGFI-2	(SER ID NO: 55)
537	TGYYTCAGAGCCATYTCNGT!	GGFI-13	(SER ID NO: 56)
538	TGYYTCCTGCGCATYTCNGT!	GGFI-13	(SER ID NO: 57)
539	CCDATHACCATGCGXAGYTT!	GGFI-17	(SER ID NO: 58)
540	GCGGCCCAACCTGRTGAC!	GGFII-1	(SER ID NO: 59)
541	GCTTCGCGYTCCTATTAATA!	GGFII-2	(SER ID NO: 60)
542	GCTTCGCTACGACGAAACCA!	GGFII-4	(SER ID NO: 61)
543	TGCGCTAARTAGCGCG!	GGFI-12	(SER ID NO: 62)
544	GCGCGXAGCGCTTCYTTNGC!	GGFI-14	(SER ID NO: 63)
545	GCGCGYAAAGCTTCYTTNGC!	GGFI-14	(SER ID NO: 64)
546	TTTITTHGCTTGACGACAA!	GGFI-15	(SER ID NO: 65)
551	TTTITTHGCTTGAAAGAA!	GGFI-15	(SER ID NO: 66)
568	TGACGACGCTTCGAC!	GGFII-8	(SER ID NO: 67)
569	TGACGAAATCTTCGAC!	GGFII-8	(SER ID NO: 68)
609	CATRTAYTCGCGGARTCGCG!	GGFII-12	(SER ID NO: 69)
610	CATRTAYTCGCGGRTCTCGCG!	GGFII-12	(SER ID NO: 70)
649	NGARTCGCGYAAAGAGCGYTT!	GGFII-12	(SER ID NO: 71)
650	NGARTCGCGYAGAGAGCGYTT!	GGFII-12	(SER ID NO: 72)
651	RGTRTCGCGYAAAGAGCGYTT!	GGFII-12	(SER ID NO: 73)
652	RGTRTCGCGYAGAGAGCGYTT!	GGFII-12	(SER ID NO: 74)
653	NGARTCGCGYAAAGCTGCGYTT!	GGFII-12	(SER ID NO: 75)
654	NGARTCGCGYAGCTGCGYTT!	GGFII-12	(SER ID NO: 76)
655	RGTRTCGCGYAAAGCTGCGYTT!	GGFII-12	(SER ID NO: 78)
656	RGTRCTGCGYAGCTGCGYTT!	GGFII-12	(SER ID NO: 79)
659	ACGACGAGATGGCTGCGCA!	GGFI-13	(SER ID NO: 80)
660	ACGACGAGATGGCTGCGCA!	GGFI-13	(SER ID NO: 81)
661	CAYCARTGTTGGCGCGGAA!	GGFII-1	(SER ID NO: 82)
662	TTYGTHGTATGAGCGGAA!	GGFII-4	(SER ID NO: 83)
663	AARGCGAGYGCNCAYACGCA!	GGFI-1	(SER ID NO: 84)
664	GARGCGYTTGCGCGYTTGAA!	GGFI-14	(SER ID NO: 85)
665	GTHCGATGCTGCGGAGTT!	GGFII-8	(SER ID NO: 86)
666	GTHCGATGCTGCGGAGTT!	GGFII-8	(SER ID NO: 87)
694	NACGTTTITTAAGAGYTTGCG!	GGFI-17	(SER ID NO: 88)

08736019-102296

Positive Series Factor II Gene Sequences

TCATAAAGTACGACATGATTTTCATGATCATATATCTGAAATATATTAAAGGCTTTGCTGCTGATCTTATGAAATTCAGAACTTCCAT 100
• G T G C I P B I I L V L • B I L E P L W S • S C C C S C L B I

TACCAAACTCTCACTGACTGATTTCTGAAATATATCTGAAATGATCAAGAAATAGCAATGCACTGCTCTGCAACATCACTTTCTGAAATCA 200
• K A S L A S C C S T B C E V I S E L C S O S A S A S I T I V S S

AACATATGATGCTGATGCTGCTATTTCTGAAATGATCAAGAAATATCTGCTCACTTCAATCACTCACTGCTGCTGAAATCTCAT 300
• G C C C L L A I S C S L E A V I E V C S R I • I S O V C S I S L

TCGAAAGTAAAGTCAATGAAAGTCTGATCTTGAATATCTATGAAATGCTCTGTAAGAACTTTCACTGATTAAGTCAATTAAGTCAAT 400
• T G E S C S E T L C L E T L A P P V E L I T P • S S I O L E

ATATATATATATTT
T I • I I

(SEQ ID NO: 89)

FIGURE 22

08736019-102296
962207-6T09E280

PCR PRIMERS FOR FACTOR I AND FACTOR II

FIGURE 23

Degenerate PCR primers

Oligo	Sequence	Peptide	
657	CCGAAATTCCTGCAGGARAHCAGCENGAYCENGGI	GGPII-17	(SEQ ID NO: 90)
658	AAGGATCCTGCAGHGTTRTANGCHCHATHACCATNGG!	GGPII-17	(SEQ ID NO: 91)
667	CCGAAATTCCTGCAGGCHGAYTCHGGNGARTAYATGI	GGPII-12	(SEQ ID NO: 92)
668	CCGAAATTCCTGCAGGCHGAYATYCHNGARTAYATI	GGPII-12	(SEQ ID NO: 93)
669	AAGGATCCTGCAGHGHHCATRTAYTCHCNGARTCI	GGPII-12	(SEQ ID NO: 94)
670	AAGGATCCTGCAGHGHHCATRTAYTCHCGRRTCTCI	GGPII-12	(SEQ ID NO: 95)
671	CCGAAATTCCTGCAGGAYCAGGTHTGGGCHGCHAA!	GGPII-1	(SEQ ID NO: 96)
672	CCGAAATTCCTGCAGATRTTYYTYYATGGARGCHGARG!	GGPII-2	(SEQ ID NO: 97)
673	CCGAAATTCCTGCAGGGGGCHGCHGCHGCHTYYCHGT!	GGPII-3	(SEQ ID NO: 98)
674	CCGAAATTCCTGCAGTGGTYYGTHTNATHGARGG!	GGPII-4	(SEQ ID NO: 99)
677	AAGGATCCTGCAGGYTTHGCHGCHGCHGCHGCHTCTCI	GGPII-1	(SEQ ID NO: 100)
678	AAGGATCCTGCAGGCHGCHGCHGCHGCHGCHGCHGCHG!	GGPII-2	(SEQ ID NO: 101)
679	AAGGATCCTGCAGGCHGCHGCHGCHGCHGCHGCHGCHG!	GGPII-3	(SEQ ID NO: 102)
680	AAGGATCCTGCAGGYTTHGCHGCHGCHGCHGCHGCHGCHG!	GGPII-4	(SEQ ID NO: 103)
681	CATRTAYTCTAYTCTCHGCHGCHGCHGCHGCHGCHGCHG!	GGPII-2	(SEQ ID NO: 104)
682	CCGAAATTCCTGCAGGARGCHGCHGCHGCHGCHGCHGCHG!	GGPII-1	(SEQ ID NO: 105)
683	GCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHG!	GGPII-14	(SEQ ID NO: 106)
684	GCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHG!	GGPII-14	(SEQ ID NO: 107)
685	TCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHGCHG!	GGPII-1	(SEQ ID NO: 108)

Unique PCR primers for Factor II

Oligo	Sequence	Comment	
711	CATCGATCTGCAGGCTGATTCTCGAGAAATATATCTGCA!	3' RACE	(SEQ ID NO: 109)
712	AAGGATCCTGCAGGCHGCHGCHGCHGCHGCHGCHGCHG!	3' RACE	(SEQ ID NO: 110)
713	CCGAAATTCCTGCAGTGAATCAAGAACTAGGAAATCA!	3' RACE	(SEQ ID NO: 111)
721	CATCGATCTGCAGGCTGATTCTCGAGAAATATATCTGCA!	5' RACE	(SEQ ID NO: 112)
722	AAGGATCCTGCAGGCHGCHGCHGCHGCHGCHGCHGCHG!	5' RACE; ANCHORED	(SEQ ID NO: 113)
723	AAGGATCCTGCAGGCHGCHGCHGCHGCHGCHGCHGCHG!	EXON A	(SEQ ID NO: 114)
726	CCGAAATTCCTGCAGGCHGCHGCHGCHGCHGCHGCHGCHG!	EXON A	(SEQ ID NO: 115)
771	CATCGGCGGCTGCAGGCHGCHGCHGCHGCHGCHGCHGCHG!	EXONS 3-4	(SEQ ID NO: 116)
772	ATACCGGCGGCTGCAGGCHGCHGCHGCHGCHGCHGCHGCHG!	EXONS 3-4	(SEQ ID NO: 117)
773	AAGGATCCTGCAGGCHGCHGCHGCHGCHGCHGCHGCHG!	ANCHORED	(SEQ ID NO: 118)
776	ATACCGGCGGCTGCAGGCHGCHGCHGCHGCHGCHGCHGCHG!	EXONS 3-4	(SEQ ID NO: 119)

08736019-102296

Summary of contiguous GGF-II cDNA structures and sequences

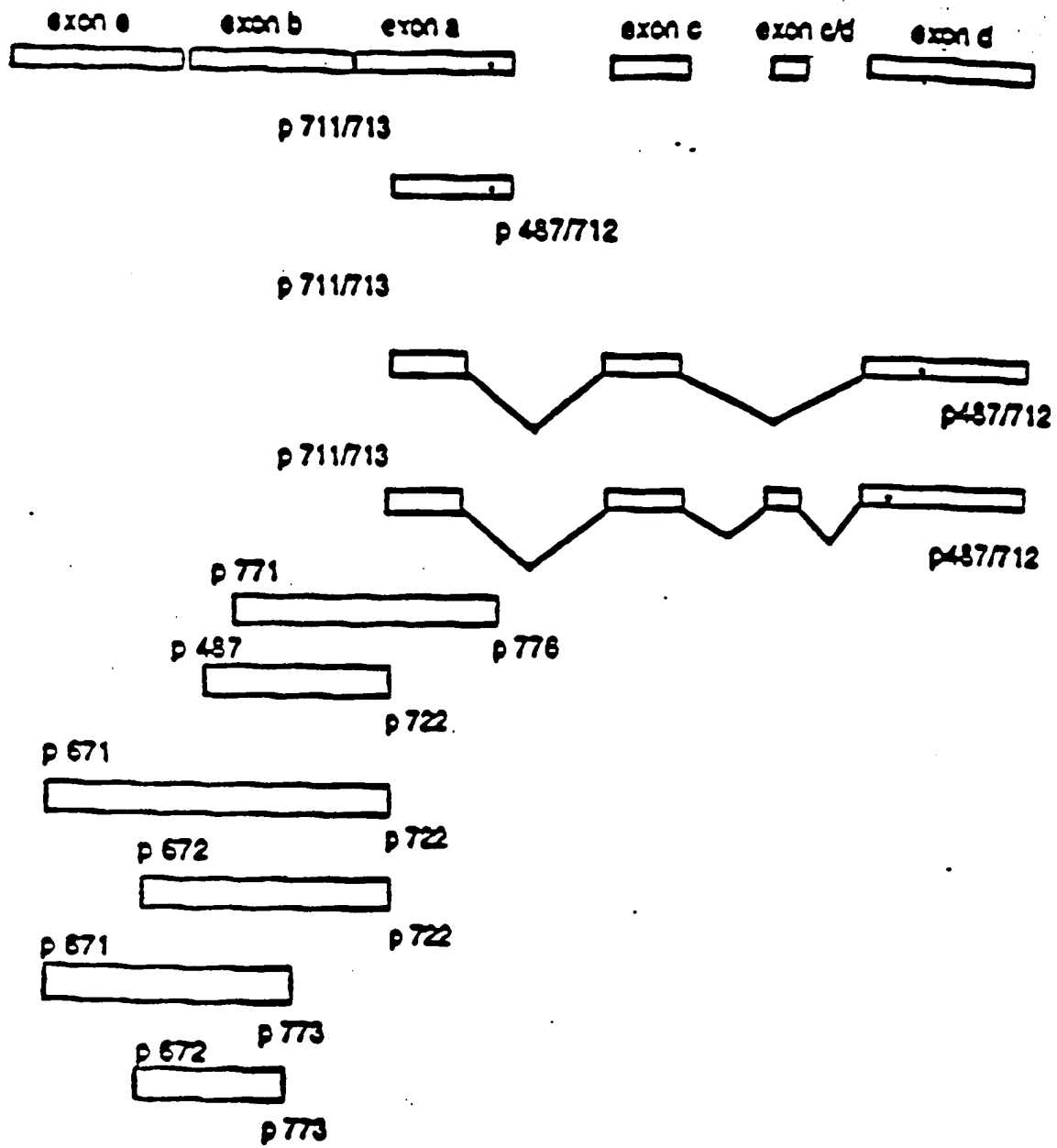
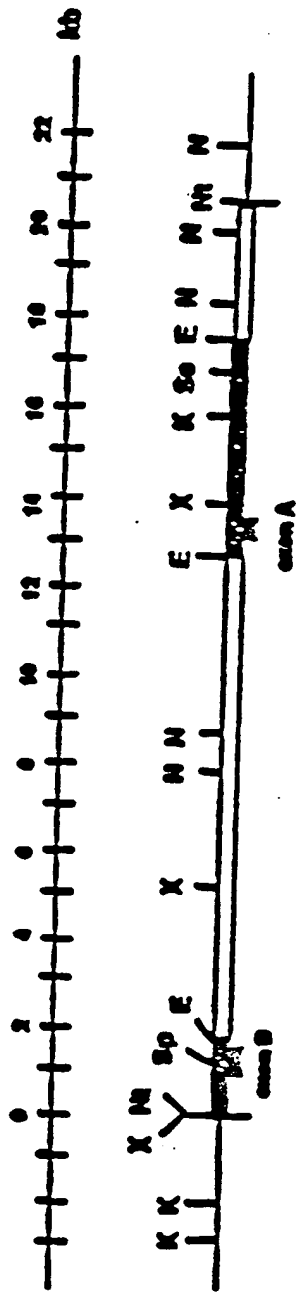


FIGURE 24

96220T 6T09E480

FIGURE 25



Alternative gene products of putative bovine GGF-2



FIGURE 26

00736019-102296

OCF-II protein identified in deduced
of putative bovine OCF-II proteins

16 sequences

Peptide	Pos.	Sequence Match	
II-1	1:	VHQVWAAX HQVWAAX AAGLR	(SEQ ID NO: 120)
II-10	14:	DLLLV GGLLV delliv RLGM.	(SEQ ID NO: 121)
II-03	21:	LGAHGPPAFPVXY LLTVR lgaughpafpvcg RLVD	(SEQ ID NO: 122) (SEQ ID NO: 123)
II-02	41:	YIFTHZPEANSSG KEDSR YIFTHZPEANSSG GPGL	(SEQ ID NO: 124) (SEQ ID NO: 125)
II-6	103:	LVLK VAGSK LVLK CETSS	(SEQ ID NO: 126)
I-18	112:	EYKCLKFKWTKQATVK CETSS eyslklfkvfkngsal SPQK	(SEQ ID NO: 127) (SEQ ID NO: 128)
II-12	151:	KASLADSGEYHCK ELRIS KASLADSGEYHCK VISKL	(SEQ ID NO: 129) (SEQ ID NO: 130)
I-07	152:	ASLADIEYHCK LRISK asladsgeyhck VISKL	(SEQ ID NO: 131) (SEQ ID NO: 132)

FIGURE 27

08736019-102296

CONFIDENTIAL 100
4000
CONFIDENTIAL 200
4000

(SEQ ID NO: 134)

FIGURE 283

0530191000



(SEQ ID NO: 135)

FILE 28C

0325039 306

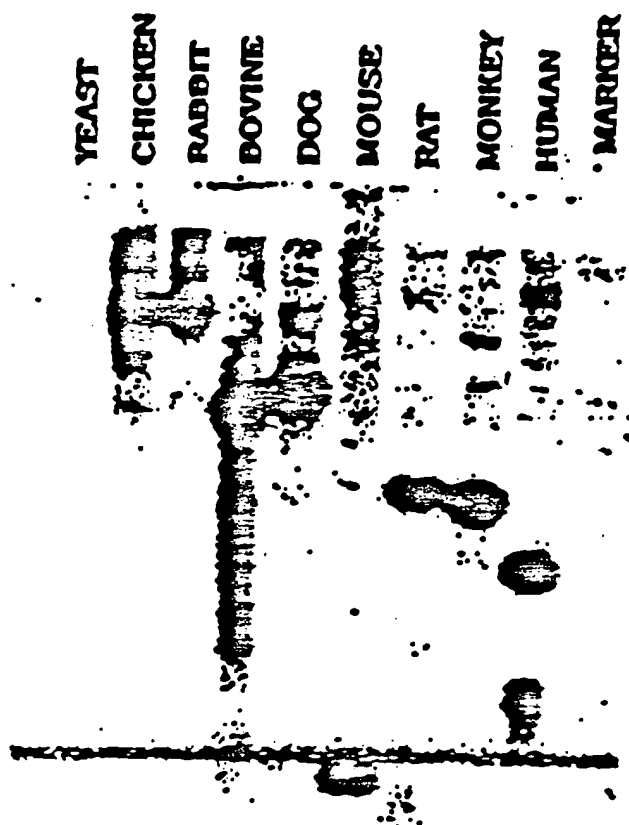
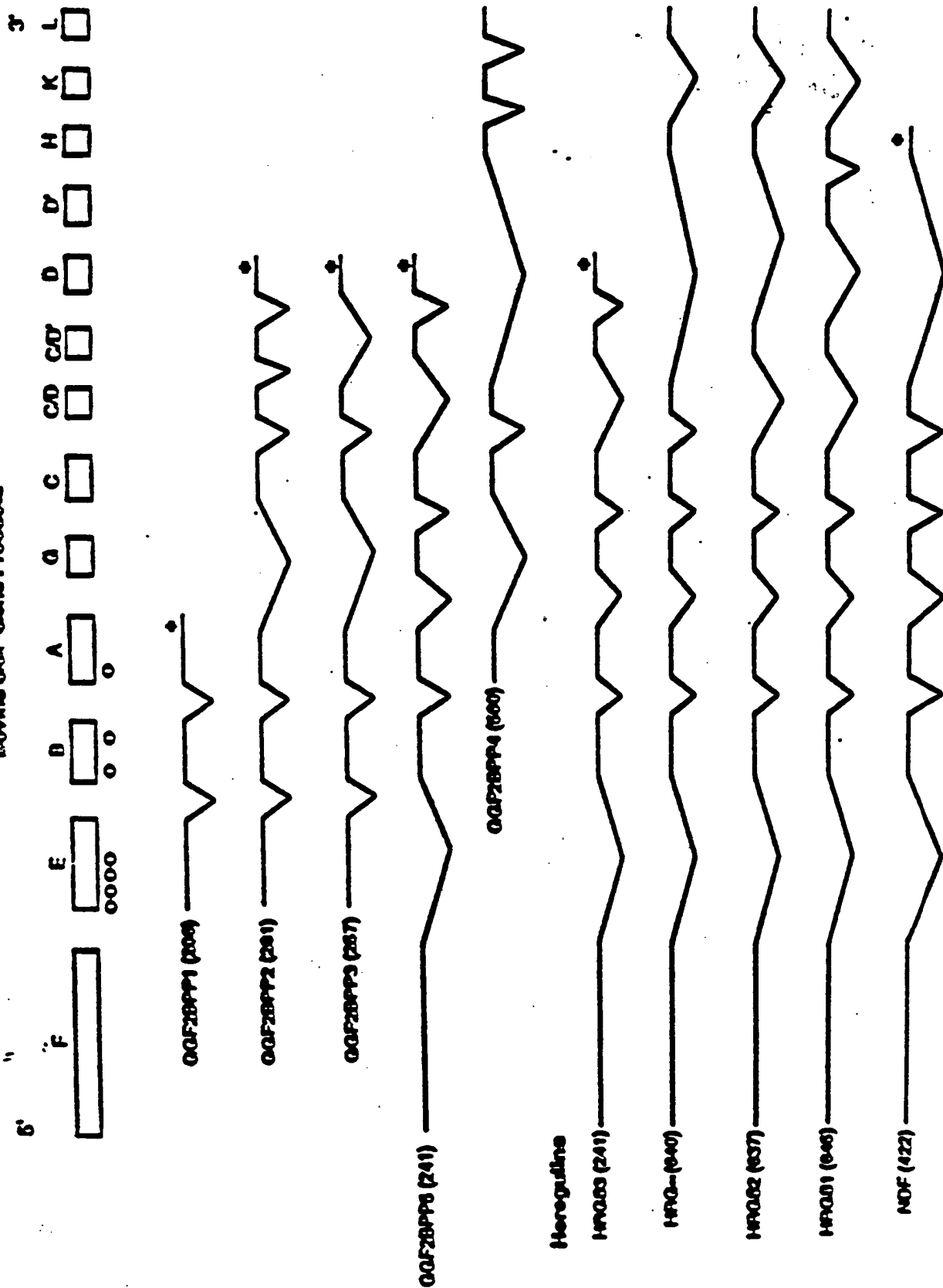


FIGURE 29

FIGURE 10

Revised GOF Gene Products



CODING SIGNATURE P: (SEQ ID NO: 136)

~~CODING SECRET 2: (SEQ ID NO: 137)~~

CCCATCAGTCTGCGGCGGCGAAGCGCGCGCTTGAGAAAGCACTCGCTGCTCAGCGTGC 60
 H Q V N A A K A G G L K K D S L L T V R
 GCGTGGCGGCGCTGCGGCGAAGCGCGCGCTTGAGAAAGCACTCGCTGCTCAGCGTGC 120
 L G A M G N P A P P S C G R L K E D S R
 GGTACATCTTCTTCAATCGAAGCGCGCGCGCTTGAGAAAGCACTCGCTGCTCAGCGTGC 180
 Y I F F H E P E A N S S G G P G R L P S
 GCCTCGCTGCGCGCGCTGCGAAGCGCGCGCGCTTGAGAAAGCACTCGCTGCTCAGCGTGC 240
 L L P P S R D G P E P Q E G G Q P G A V
 TCGAAGCGCTGCG 252

FIGURE 31 (CONT.)

CODING SEGMENT B: (SEQ ID NO: 138)

L P P R L K E N K S Q E S V A G S K L V
 CCTTGCCTCCCGCCTTGAAGAGATGAAGACTCAGGAGTCTGTGCGACGTTCCAACTAG 60
 |||||
 ccttgcctcccgattgaaagagatgaaagccagggaatcggtgcagggtccaaactag
 Q A

 L R C E T S S E Y S S L K F I V P K N G
 TCCTTCGCTCCGACAGCCAGTTCTCAATACTCCTCTCTCAAGTTCAAGTCTTCAAGAAATC 120
 |||||
 tccttcggtgtgaaaccagttctgataactcctctctcagattcaagtgttcaagaatg
 R

 S E L S R K N K P Q N I K I Q K R P G
 CGAGTGAATTAAGCCCAAGCAACCAACCAACATCAAGATACAGAAAGCCCCCG 178
 |||||
 ggaatgaattgaatcgaaaaaaccaaccacaaaatatcaagatacaaaaaagccagg
 M N X

CODING SEGMENT A: (SEQ ID NO: 139)

K S E L R I S K A S L A D S G E Y N C K
 GAAGTCAGAACTTCCGATTAGCAAGCGTCACTGGCTGATTCTGCAGAAATATATGTGCA 60
 |||||
 gaagtcaagacttcgcattcaaaagcatcactgggtgattctggagagtatatgtgcaa
 N

 V I S K L G N D S A S A N I I V E S N
 AGTGATCAGCAAACTAGCAAAATCAAGTCCCTCTGCCAAACATCAACATTGTGAGTCAA 120
 |||||
 agtgatcagcaaaattaggaattgacgtgacctctgccaatatcaccaatctgggaatcaa
 A
 CG 122
 ||
 CG

CODING SEGMENT A': (SEQ ID NO: 140)

TCTAAAACTACAGAGACTGTATTTCATGATCATCATAGTTCTGTCAAAATATACTTAAAC 60

 K S E L R I S K A S L A D
 CGCTTTGGTCTCTGATCTTGTAGCAAGTCAGAACTTCCGATTAGCAAGCGTCACTGGCTC 120

 S G E Y N C K V I S K L G N D S A S A N
 ATTCTGCAGAAATATATGTGCAAACTGATCAGCAAACTAGCAAAATCAAGTCCCTCTGCCA 180

 I T I V E S N G K R C L L R A I S Q S I
 ACATCACCATTGTCCAGTCAAAAGCTAAGAGATGCCCTACTGCCGTGCTATTCTCAGTCTC 240

 R G V K V C E N
 TAAAGAGAGTCAATCAAGTATGTCTCTCACTTTCAATCAGCCAGGTCTGTGAAATCTCAT 300

08736019-102296

TGTCACAAATAAATCAATGAAAGGAAATCTCTATGTTTCAAAATATCTTATGGGTCTC 360
 CTGTAAAGCTCTTCACTCCATAAGGTCAAATAGACCTCAAAATATATATAGATTATTT 417

CODING SEGMENT G: (SEQ ID NO: 141)

E I T T G N P A S T E T A Y V S S E S P I 60
 AGATCACCACCTGCAATGCCAGCCTCACTGAGACAGCCTATCTGCTCTTCAGAGTCTCCCA
 |||||
 agatcatcactggtatgccaagcctcaactgaaggagcatatgtgtcttcagagtctccca

R I S V S T E G T N T S S S 102
 TTAGAAATATCACTATCAACAGAAAGCAAAATACTTCTTCAAT
 |||||
 ttagaataatcagtatccacagaaaggagcaataacttcttcat

CODING SEGMENT G: (SEQ ID NO: 160)

T S T S T A G T S E L V K C A E K E K I 60
 CCAATCCACATCTACAGCTGGGACAAAGCCATCTTGTCAAGTCTCCAGACAAAGCAAAA
 |||||
 ctacatctacatccaccactgggacaaagccatcttgtaaaaatgtgcggagaaaggagaaaa

F C V N G G E C F N V K D L S N P S R Y 120
 CTTTCTCTCTCAATCCAGCCCACTGCTTCAATGCTCAAACACCTTTCAAAATCCCTCAAGAT
 |||||
 ctttctctctgaatggaggggagtgcttcatgggtgaagacctttcaaacccctcgagat

L C 128
 ACTTCTCC
 |||||
 acttctgc

FIGURE 31 (CONT.)

CODING SEGMENT C/D: (SEQ ID NO: 142)

K C Q P G F T G A R C T E N V P N K V Q 60
 AACTGCCAAACCTGGATTCACTGGAGCGAGATGTACTGAGAAATGTGCCCATGAAAGTCCAA
 |||||
 aagtgccaaacctggattcactggagcagagtggtactgagaatgtgcccatgaaagtccaa

T Q E
 ACCCAAGAA 69
 |||||
 aaccaagaa
 N

CODING SEGMENT C/D': (SEQ ID NO: 143)

K C P N E F T G D R C Q N Y V N A S F Y 60
 AACTGCCCAAATGAGTTTACTGGTCAATGGCTGCCAAAATACGTAATGCCCAAGCTTCTAC
 |||||
 aagtgcccaaatagagtttactggatgagctgccaaaactacgtaatggccagcttctac

CODING SEGMENT D: (SEQ ID NO: 144)

S T S T P F L S L P E 36
 AGTACGTCCACTCCCTTTCTGTCTCTGCTTGAATAG
 |||||
 agtacgtccactccctttctgtctctgcttgaatag

CODING SEGMENT D': (SEQ ID NO: 145)

K E L G I E P N E
 aagcatcttgggattgaatttatggag 27

06736019-102296

SECRET

K A E E L Y Q K R V L T I T G I C I A L 60
 A A C C C G A C C A G C T C T A C C A G A A G A C A G T G C T C A C C A T T A C C G C C A T T T G C A T C G C C G T G
 A A G G C G G A G G A G C T G T A C C A G A A G A G A G T G C T G A C C A T A A C C G G C A T C T G C A T C G C C T C
 L V V G I N C V V V Y C K T K K Q R K K 120
 C T C G T C C T T G C C A T C A T G T G T G T C C T G C T A C T G C A A A C C A G A A A C A A C C G A A A A G
 C T T G T G G T C G G C A T C A T G T G T G T G G G C T A C T G C A A A C C A A G A A A C A G C G G A A A A A G
 L H D R L R Q S L R S E R N T N N N V A 180
 C T T C A T G A C C C C C T T G C C A C A G C C T T C C C T G T G A A A C A A A C A C C A T C A T G A A C G T A G C C
 C T G C A T G A C C C T C T T C G G C A G A G C C T T C G G T C T G A A C G A A A C A T A T G A T G A A C A T T G C C
 K C P H E P N P P P E N V Q L V N Q Y V 240
 A A C C G C C C C C A C C A C C C C A T C C G C C C C C C A G A A C G T G C A G C C T G C A A T C A A T A C G T A
 A A T G G G C C T C A C C A T C C T A A C C C A C C C C C G A G A A T G T C C A G C T G G T G A A T C A A T A C G T A
 S K N V I S S E N I V E R E A E S S P S 300
 T C T A A A A T G T C A T C T C T A C C G A C C A T A T T G T T G A C A G A G A G C C G C C A G A G C C T C T T T T T C C
 T C T A A A A C G T C A T C T C C A G T G A G C A T A T T G T T G A G A G A G A G C A G A G A C A T C C T T T T C C
 T S H Y T S T A N H S T T V T Q T P S E 360
 A C C A G T C A C T A C A C T T G C A C A C C T C A T C A T T C C A C T A C T G T C A C T C A G A C T C C C A G T C A C
 A C C A G T C A C T A T A C T T C C A C A G C C C A T C A C T C C A C T A C T G T C A C C C A G A C T C C T A G C C A C
 S W S N G H T E S I I S E S E S V I V N 420
 A C C T G C A C C A T G C A C A C A C T G A A A C A T C A T T T C C G A A A C C C A C T G T G T C A T C C T G A T C
 A G C T G G A G C A A C G G A C A C A C T G A A A G C A T C C T T T C C G A A A G C C A C T C T G T A A T C G T G A T G
 S S V E N S R E S S P T G G P R G R L N 480
 T C A T C C C T A C A A A C A G T A C C C A C A C C A C C C C A C T G C C C C C C C A C A G C C C T C A A T
 T C A T C C G T A G A A A C A G T A G G C A C A G C A G C C C A A C T G G G G G C C C A A G A G G A C G T C T T A A T
 G L G G P R E C N S P L R N A R E T P D 540
 G C C T T G C C A G C C C C C T G T G A A T G T A A C A G C T T C C T C A C C C A T C C C A G A G A A C C C C T G A C
 G G C A C A G G A G G C C C T C G T G A A T G T A A C A G C T T C C T C A G G C A T G C C A G A G A A A C C C C T G A T
 S Y R D S P H S E R 569
 T C C T A C C G A G A C T C T C C T C A T A G T G A A A C
 T C C C A C C G A G A C C C C C A T A G T G A A A G

CODING SEGMENT K: (SEQ ID NO: 161)

ACATAACCTTATAGCTGAGCTAAGGAGAAACAGGCCCAACAGATCCAAATGATCCAGAT
 H N L I A E L R R N K A N R S K C N Q I
 CCAAGCTTTCCGCAACTCATCTTACAGCTTCTTCCATTCCCCATTGGGCTTCATTCTCTAA
 Q L S A T N L R A S S I P N N A S F S K
 CACCCCTTGGCCTTLAGCAAG
 T P N P L G R

CODING SEGMENT L: (SEQ ID NO: 147)

Y V S A N T T P A R N S P V D F N T P S
 GTATGTATCAGCAATGACCAACCCCTCTCTATGTACCTGTAGATTTCACACCCCAAG 60
 GTATGTGTGAGCCATGACCAACCCCTCTCTATGTACCTGTAGATTTCACACCCCAAG
 S P K S P P S E N S P P V S S T T V S N
 CTCCCCCAAGTCAACCCCTCTCTGAAATGTCCCCCTCTCTCAGCAACCAACCTCTCTCA 120
 CTCCCCCAAGTCAACCCCTCTCTGAAATGTCCCCCTCTCTCAGCAACCAACCTCTCTCA
 P S K A V S P P V E E E R P L L L V T P
 GCGCTCCATGGCGCTCAGTCCCTCTCTGAAAGAGAGAGACCCCTCTCTCTCTGACCCC 180
 GCGCTCCATGGCGCTCAGTCCCTCTCTGAAAGAGAGAGACCCCTCTCTCTCTGACCCC
 P R L R E K Y D E N A Q Q P N S P E C
 ACCACCGCTGCGGCAAG...TATCAACCAACCAACCAACCAATTCAACTCTCTCACTG 240
 ACCACCGCTGCGGCAAG...TATCAACCAACCAACCAACCAATTCAACTCTCTCACTG
 E P A N E S N S L P P S P L R I V E D E
 CAAACCCCTGCTGAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 300
 CAAACCCCTGCTGAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA
 E Y E T T Q E Y E P A Q E P V K K L T N
 CGAATATGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 360
 CGAATATGAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA
 S S R R A K R T K P N G H I A N R L E N
 CAGCAGCCCGCGCGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 420
 CAGCAGCCCGCGCGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA
 ...TAGCGGCGCGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA

733

09-03-2017

Figure 1. The effect of the concentration of the *Agrobacterium* strain on the transformation efficiency of *Agrobacterium* strain 1024. The *Agrobacterium* strain 1024 was cultured in the YEA medium for 24 h at 28°C. The cell concentration was adjusted to 1.0 × 10⁸ cells/ml. The cell suspension was mixed with the cell suspension of the *Agrobacterium* strain 1024 at the ratio of 1:1, 1:2, 1:3, 1:4, 1:5, 1:6, 1:7, 1:8, 1:9, 1:10, 1:15, 1:20, 1:30, 1:40, 1:50, 1:60, 1:70, 1:80, 1:90, 1:100, 1:150, 1:200, 1:300, 1:400, 1:500, 1:600, 1:700, 1:800, 1:900, 1:1000, 1:1500, 1:2000, 1:3000, 1:4000, 1:5000, 1:6000, 1:7000, 1:8000, 1:9000, 1:10000, 1:15000, 1:20000, 1:30000, 1:40000, 1:50000, 1:60000, 1:70000, 1:80000, 1:90000, 1:100000, 1:150000, 1:200000, 1:300000, 1:400000, 1:500000, 1:600000, 1:700000, 1:800000, 1:900000, 1:1000000, 1:1500000, 1:2000000, 1:3000000, 1:4000000, 1:5000000, 1:6000000, 1:7000000, 1:8000000, 1:9000000, 1:10000000, 1:15000000, 1:20000000, 1:30000000, 1:40000000, 1:50000000, 1:60000000, 1:70000000, 1:80000000, 1:90000000, 1:100000000, 1:150000000, 1:200000000, 1:300000000, 1:400000000, 1:500000000, 1:600000000, 1:700000000, 1:800000000, 1:900000000, 1:1000000000, 1:1500000000, 1:2000000000, 1:3000000000, 1:4000000000, 1:5000000000, 1:6000000000, 1:7000000000, 1:8000000000, 1:9000000000, 1:10000000000, 1:15000000000, 1:20000000000, 1:30000000000, 1:40000000000, 1:50000000000, 1:60000000000, 1:70000000000, 1:80000000000, 1:90000000000, 1:100000000000, 1:150000000000, 1:200000000000, 1:300000000000, 1:400000000000, 1:500000000000, 1:600000000000, 1:700000000000, 1:800000000000, 1:900000000000, 1:1000000000000, 1:1500000000000, 1:2000000000000, 1:3000000000000, 1:4000000000000, 1:5000000000000, 1:6000000000000, 1:7000000000000, 1:8000000000000, 1:9000000000000, 1:10000000000000, 1:15000000000000, 1:20000000000000, 1:30000000000000, 1:40000000000000, 1:50000000000000, 1:60000000000000, 1:70000000000000, 1:80000000000000, 1:90000000000000, 1:100000000000000, 1:150000000000000, 1:200000000000000, 1:300000000000000, 1:400000000000000, 1:500000000000000, 1:600000000000000, 1:700000000000000, 1:800000000000000, 1:900000000000000, 1:1000000000000000, 1:1500000000000000, 1:2000000000000000, 1:3000000000000000, 1:4000000000000000, 1:5000000000000000, 1:6000000000000000, 1:7000000000000000, 1:8000000000000000, 1:9000000000000000, 1:10000000000000000, 1:15000000000000000, 1:20000000000000000, 1:30000000000000000, 1:40000000000000000, 1:50000000000000000, 1:60000000000000000, 1:70000000000000000, 1:80000000000000000, 1:90000000000000000, 1:100000000000000000, 1:150000000000000000, 1:200000000000000000, 1:300000000000000000, 1:400000000000000000, 1:500000000000000000, 1:600000000000000000, 1:700000000000000000, 1:800000000000000000, 1:900000000000000000, 1:1000000000000000000, 1:1500000000000000000, 1:2000000000000000000, 1:3000000000000000000, 1:4000000000000000000, 1:5000000000000000000, 1:6000000000000000000, 1:7000000000000000000, 1:8000000000000000000, 1:9000000000000000000, 1:10000000000000000000, 1:15000000000000000000, 1:20000000000000000000, 1:30000000000000000000, 1:40000000000000000000, 1:50000000000000000000, 1:60000000000000000000, 1:70000000000000000000, 1:80000000000000000000, 1:90000000000000000000, 1:100000000000000000000, 1:150000000000000000000, 1:200000000000000000000, 1:300000000000000000000, 1:400000000000000000000, 1:500000000000000000000, 1:600000000000000000000, 1:700000000000000000000, 1:800000000000000000000, 1:900000000000000000000, 1:1000000000000000000000, 1:1500000000000000000000, 1:2000000000000000000000, 1:3000000000000000000000, 1:4000000000000000000000, 1:5000000000000000000000, 1:6000000000000000000000, 1:7000000000000000000000, 1:8000000000000000000000, 1:9000000000000000000000, 1:10000000000000000000000, 1:15000000000000000000000, 1:20000000000000000000000, 1:30000000000000000000000, 1:40000000000000000000000, 1:50000000000000000000000, 1:60000000000000000000000, 1:70000000000000000000000, 1:80000000000000000000000, 1:90000000000000000000000, 1:100000000000000000000000, 1:150000000000000000000000, 1:200000000000000000000000, 1:300000000000000000000000, 1:400000000000000000000000, 1:500000000000000000000000, 1:600000000000000000000000, 1:700000000000000000000000, 1:800000000000000000000000, 1:900000000000000000000000, 1:10

(SEQ ID NO: 163)

[illegible]

GGP2BPP5 nucleotide sequence and deduced protein sequence

AGTTTCCCCCCCCAACTTGTCCAACTCTCCCTCCGCGCCAGGGCAGGAGCCGAGCCG 60
 GCGCCCTGCTCCAGGCCATGCTCAGCCGCGGCGGCGGAGCCGTAATCCGCTCTCTCTCTCCG 120
 TCCTAGCCCTCCCGGACCCAGCCAGCCAGCCAGCCGACCCGCGCGGGAACCCAGGACTCC 180
 CCAAGCCGCGCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 240
 ACTCCCAAGCTGCGCGGCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 300
 GCTCCCCCGGAGCCGCGCGGCGGCTCCGCGCGGCTCCGCTCCGCGCGGCTCCAGCCAGCC 360
 AACTTTTCTCCGGAAGCCAGCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 420
 CCGGAGCCGCTCCGCGCGGCGGAGCCGCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 480
 M S E R R E G
 AAGCCAGGCGGGAAGCCGCGGCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 540
 K G K G K G G K K D R G S G K K P V P A
 GCTCGCGCGGCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 600
 A C G P S P A L P P R L K E H K S Q E S
 GTCCAGCCGTTCCAACTAGCTCTCCGCGGCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCC 660
 V A G S K L V L R C E T S S E Y S S L K
 TTCAGCTGCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 720
 F K M P K M G S E L S R K N K P Q H I K
 ATACAGAAAGCCGCGGCGGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC 780
 I Q K R P G K S E L R I S K A S L A D S
 GAGCAATATATGTCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 840
 G E Y M C K V I S K L G H D S A S A H I
 ACCATTCTGCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 900
 T I V E S H E I T T G M P A S T E T A Y
 GTGCTCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 960
 V S S E S P I R I S V S T E G T H T S S
 TCCAGCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1020
 S T S T S T A G T S H L V K C A E K E K
 ACTTTCTGCTGTAATCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1080
 T P C V M G G E C P M V K D L S H P S R
 TACTGCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1140
 Y L C K C P M E P T G D R C Q H Y V M A
 AGCTTCTACAGTACCTCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1200
 S F Y S T S T P F L S L P E
 GTCCGCGGCT 1260
 CT 1320

08736019-102296

FIGURE 32 (CONT.)

TGA CTTCCTCTCTCCGTCACTAGTGGGCTCTGAGCTACTCGTAGCCTAAGGCTCCAG 1380
 TGTTCCTCAATTCATCTTCAATTA CTGTCTATAGGACATCATAGTCCCTCTCA CCGCAGTG 1440
 CAATGACAAATAAAGGCTTCAAAAAGTCTCACTTTTATTGAGAAAATAAAAATCGTTCCAG 1500
 GCGACAGTCCCTCTTCTTTATAAAATGACCTATCTTGA AAAAGGAGGTCTGTAAAGTTG 1560
 TAAACCACTACACACTTCAAAATCATCTAAAGTTCCGCTTCCGTTCA GAAATCTCTTCTTCTG 1620
 ACAATAAACAGAAATAAAAAA 1653

08735019-102296

GGP2BPP2 nucleotide sequence and deduced protein sequence

CATCATGTGTGGGCGGCGAAGCGGCGGCGGCTTCAAGAACTCGCTGCTCAAGCTGCGG 60
 H Q V W A A K A G G L K K D S L L T V R
 CTGCGGCGGCTGGGCGGCAAGCGGCGGCTTGGGCTGCTGCGGCGGCTCAAGCGGCAAGCGG 120
 L G A N G H P A P P S C G R L K S D S R
 TACATGTTTTCATGCAAGCGGCGGCAAGCGGCGGCGGCTGCGGCGGCGGCTTGGGCGG 180
 Y I P P H E P E A N S S G G P G R L P S
 CTGCTTGGGCGGCTTCAAGCGGCGGCAAGCTTCAAGAACTCGCTCAAGCGGCGGCTGCTG 240
 L L P P S R D G P E P Q E G G P G A V
 CAAGCTGCGGCTTGGGCTGCGGCTTCAAGCGGCGGCAAGCTTCAAGCGGCTGCTGCGGCGG 300
 Q R C A L P P R L I E H K S Q E S V A G
 TCCAACTAGTGTGCTGCGGCGGCAAGCTTCAAGAACTCGCTTCAAGCTTCAAGCTGCGG 360
 S K L V L R C E T S S E Y S S L K P K N
 CTCAACTAGTGTGCGGCGGCAAGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAG 420
 P K N G S E L S R I N K P E H I E I Q K
 ACGCGGCGGCAAGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAGCGGCGGCTT 480
 R P G K S E L R I S K A S L A D S G E Y
 ATGTGCGGCGGCAAGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAGCGGCGGCT 540
 K C K V I S K L G H D S A S A H I T I V
 GAGTCAAGCGGCGGCAAGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAGCGGCG 600
 E S N A T S T S T A G T S E L V K C A E
 AAGCGGCGGCAAGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAGCGGCGGCTT 660
 K E K T P C V H G G E C P H V K D L S N
 CCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAGCGGCG 720
 P S R Y L C K C Q P G P T G A R C T E H
 GTGCGGCGGCAAGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAGCGGCGGCTT 780
 V P H K V Q T Q E E C P H E P T G D R C
 CAAGCTAGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCA 840
 Q H Y V H A S P Y S T S T P P L S L P E
 TAGCGCATCTCAAGCTGCGGCGGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAG 900
 AAGCTAGCTGCGGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAGCGGCGGCTT 960
 AACACAAAGCGGCTTCAAGCTGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAGCGGCGGCT 1020
 GTGCGGCGGCAAGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAGCGGCGGCTT 1080
 TCGGCTCAAGCGGCTTCAAGCGGCGGCAAGCTTCAAGCGGCGGCTTCAAGCGGCGGCTT 1140

08736019-102296

GGF2BPP4 nucleotide sequence and deduced protein sequence

GAAGTCAGAACTTCCATTAGCAAGCGTCACTGGCTCAATTCTGCAGAAATATGTGCA 60
 K S E L R I S K A S L A D S G E Y M C K
 AGTCATCAGCAAACTAGCAATGACAGTGCCTCTGCCAACATCACCATTGTGGAGTCA 120
 V I S K L G N D S A S A N I T I V E S N
 CGCCACATCCACATCTACAGCTGGCAAGCCATCTTGTCAAGTGTGCAGAGAGGAGAA 180
 A T S T S T A G T S E L V K C A E K E K
 AACTTTCTGTGTGAATGGAGCGGACTGCTTCATGGTGAAAGACCTTTCAATCCCTCAAG 240
 T F C V N G G D C F M V K D L S N P S R
 ATACTTCTCAAGTGCCAACCTGGATTCACTGGAGCCAGATGTACTGCAATGTGCCCAT 300
 Y L C K C Q P G F T G A R C T E N V P M
 GAAAGTCCAAACCCAGAAAGAGCGGAGGAGCTGTACCAAGAGAGAGTGCCTCACCATTAC 360
 K V Q T Q E K A E E L Y Q K R V L T I T
 CGGCATTTGCAATCGCGCTGCTGCTGCTTGGCATCATGTGTCTGCTGCTTACTGCCAAAC 420
 G I C I A L L V V G I N C V V V Y C K T
 CAAGCAACAAACGAAAGGCTTCATGACCGGCTTCCGCAAGGCTTCCGCTCTCAAGAA 480
 K K Q R K K L E D R L R Q S L R S E R N
 CACCATGATCAACCTAGCCAAACGTCGCCCAACCAACCAATCCGCCCCCGAGAACCTGCC 540
 T M N N V A N G P H E P N P P P E N V Q
 CCTGCTCAATCAATACGTATCTAAAAATGTCACTCTTAGCCAGCATATTGTTGAGAGAG 600
 L V N Q Y V S K N V I S S E H I V E R E
 GCGGAGAGCTCTTTTTCACCACTCACTACACTTCCACAGCTCATCATTCCTACTCTGT 660
 A E S S F S T S E Y T S T A E E S T T V
 CACTCAGACTCCCACTCAAGCTCCAGCAATGGACACACTCAAGCATATTTCGCAAG 720
 T Q T P S E S M S N G H T E S I I S E S
 CCACTCTGTCACTCTCATCTCATCCCTAGCAAAACAGTAGCCACAGCAGCCCCCACTGGGG 780
 H S V I V N S S V E N S R E S S P T G G
 CCCCACAGGACCTCTCAATGGCTTGGAGCGCCCTCTCAATGTAAACAGCTTCTCAGCC 840
 P R G R L N G L G G P R E C H S P L R E
 TGCCACAGCAACCCCTCACTCTTACCGAGACTCTCTCTCATAGTCAAGACATAACCTTAT 900
 A R E T P D S Y R D S P H S E R E N L I
 AGCTGAGCTAAGGAGAAACAGGCCCCACAGATCCAAATGCAAGCAGATCCAGCTTTCCGC 960
 A E L R R N K A E R S K C M Q I Q L S A
 AACTCATCTTAGAGCTTCTTCCATTCCCCATTGGGCTTCAATTCTTAAGACCCCTTGGCC 1020
 T H L R A S S I P H W A S F S K T P W P
 TTLAGCAAGCTATCTATCAGCAATGACCACCCCGGCTCTATGTACCTGTAGATTTCCA 1080
 L C R Y V S A M T T P A R M S P V D F H
 CACCCCAAGCTTCCCAAGTCAACCCCTTCCGAAATGTCTCTTCCCTCTTCAAGCAGGAC 1140
 T F E S F K S F P S E M S P P V S S T T

08736019-102296

FIGURE 34 (CONT.)

GGTCTCCATGCCCTCCATGCGCGTCACTCCCTTCTGGAAGAGGAGAGACCCCTGCTCTT 1200
 V S K P S K A V S P F V E E E R P L L L
 TGTACGGCCACCACTGGCTGCGGAGAACTATGACCACCAAGCCCCAGCAATTCACTCTT 1260
 V T P P R L R E K Y D H H A Q Q F N S F
 CCACTGCAACCCCGCGCATGAGAGCAACAGCCTGCCCCCAGCCCCCTGAGGATAGTGG 1320
 H C N P A H E S N S L P P S P L R I V E
 GCAATGACCAATATGAAACGACCCAGAGTACCAACCAAGCTCAAGAGCCCGTTAAGAACT 1380
 D E E Y E T T Q E Y E P A Q E P V K K L
 CACCAACAGCAGCCCGCGGCGGCAAAAGCAAGCCCAATGCTCAATTGCCACAGCTT 1440
 T N S S R R A K R T K P N G H I A E R L
 GCAATGCAACCAACCAACAGCCCGCTGACAGCAGTAACTCAGAGAGCGAAACAGAGGATCA 1500
 E N D N N T G A D S S N S E S E T E D E
 AAGAGTAGGAGCAAGATACGCGCTTCTGCGCCATACAGAAACCCCTGCGCAGCCAGTCTCA 1560
 R V G E D T P P L A I Q N P L A A S L E
 GCGCGCGCGCTGCGCTTCCCGCTGCTGCAACAGGAGTAAACCAACAGCGCGCTTCTCTCC 1620
 A A P A F R L V D S R T N P T G G F S P
 GCAGCAAGCAATTGCAAGCCAGCGCTCTCGCTGTAATCGCTAACCAAGACCGCTATCGCTGT 1680
 Q E E L Q A R L S G V I A N Q D P I A V
 CTAAACCGAAATACACCCATAGATTCACTGTAAAACTTTATTTTATATATAAAGTAT 1740
 TCCACCTTAATTAAACAAAA 1764

08736019-102296

FIGURE 35

GGF2~~MS~~KCAEKEKTFCVNGGECFMYKDLSNPSRYLCKCPNEFTGDRCQHYVMASFY¹
GGF2~~MS~~KCAEKEKTFCVNGGDCFMYKDLSNPSRYLCKCQPGFTGARCTENVPMKVQ²
DEGE ECLRKYKDFCIH - GECKYKELRAPS — CKCQOEYFGERCGEKSNTHS³

¹(SEQ ID NO: 151)

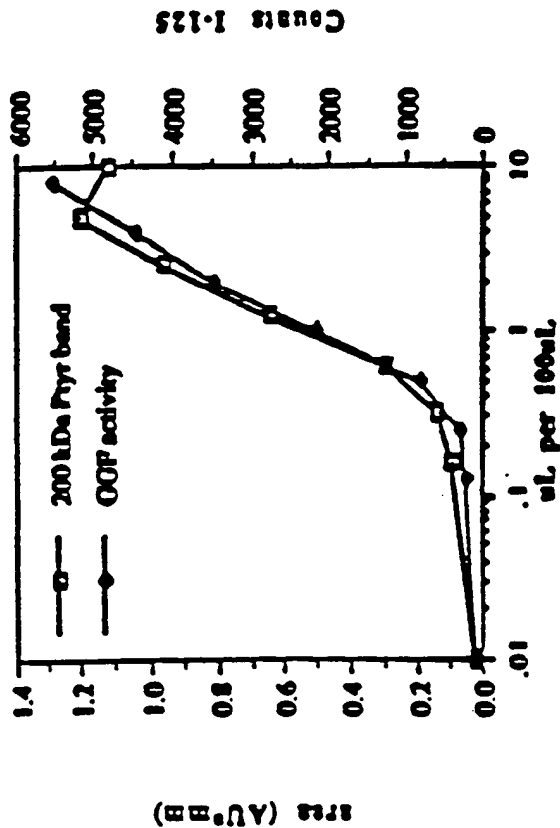
²(SEQ ID NO: 152)

³(SEQ ID NO: 153)

08736019-102296

FIGURE 36

200 kDa tyrosine phosphorylation compared with mitogenic activity



GGT/HERPESVIRUS SPLICING VARIANTS

Y-B-A'

Y-B-A-C-C/D-D
 Y-B-A-C-C/D-H
 Y-B-A-C-C/D-H-L
 Y-B-A-C-C/D-H-K-L
 Y-B-A-C-C/D-D'-H
 Y-B-A-C-C/D-D'-H-L
 Y-B-A-C-C/D-D'-H-K-L
 Y-B-A-C-C/D'-D
 Y-B-A-C-C/D'-H
 Y-B-A-C-C/D'-H-L
 Y-B-A-C-C/D'-H-K-L
 Y-B-A-C-C/D'-D'-H
 Y-B-A-C-C/D'-D'-H-L
 Y-B-A-C-C/D'-D'-H-K-L
 Y-B-A-C-C/D-C/D'-D
 Y-B-A-C-C/D-C/D'-H
 Y-B-A-C-C/D-C/D'-H-L
 Y-B-A-C-C/D-C/D'-H-K-L
 Y-B-A-C-C/D-C/D'-D'-H
 Y-B-A-C-C/D-C/D'-D'-H-L
 Y-B-A-C-C/D-C/D'-D'-H-K-L

Y-B-A-G-C-C/D-D
 Y-B-A-G-C-C/D-H
 Y-B-A-G-C-C/D-H-L
 Y-B-A-G-C-C/D-H-K-L
 Y-B-A-G-C-C/D-D'-H
 Y-B-A-G-C-C/D-D'-H-L
 Y-B-A-G-C-C/D-D'-H-K-L
 Y-B-A-G-C-C/D'-D
 Y-B-A-G-C-C/D'-H
 Y-B-A-G-C-C/D'-H-L
 Y-B-A-G-C-C/D'-H-K-L
 Y-B-A-G-C-C/D'-D'-H
 Y-B-A-G-C-C/D'-D'-H-L
 Y-B-A-G-C-C/D'-D'-H-K-L
 Y-B-A-G-C-C/D-C/D'-D
 Y-B-A-G-C-C/D-C/D'-H
 Y-B-A-G-C-C/D-C/D'-H-L
 Y-B-A-G-C-C/D-C/D'-H-K-L
 Y-B-A-G-C-C/D-C/D'-D'-H
 Y-B-A-G-C-C/D-C/D'-D'-H-L
 Y-B-A-G-C-C/D-C/D'-D'-H-K-L

Y-Z-B-A'

Y-Z-B-A-C-C/D-D
 Y-Z-B-A-C-C/D-H
 Y-Z-B-A-C-C/D-H-L
 Y-Z-B-A-C-C/D-H-K-L
 Y-Z-B-A-C-C/D-D'-H
 Y-Z-B-A-C-C/D-D'-H-L
 Y-Z-B-A-C-C/D-D'-H-K-L
 Y-Z-B-A-C-C/D'-D
 Y-Z-B-A-C-C/D'-H
 Y-Z-B-A-C-C/D'-H-L
 Y-Z-B-A-C-C/D'-H-K-L
 Y-Z-B-A-C-C/D'-D'-H
 Y-Z-B-A-C-C/D'-D'-H-L
 Y-Z-B-A-C-C/D'-D'-H-K-L
 Y-Z-B-A-C-C/D-C/D'-D
 Y-Z-B-A-C-C/D-C/D'-H
 Y-Z-B-A-C-C/D-C/D'-H-L
 Y-Z-B-A-C-C/D-C/D'-H-K-L
 Y-Z-B-A-C-C/D-C/D'-D'-H
 Y-Z-B-A-C-C/D-C/D'-D'-H-L
 Y-Z-B-A-C-C/D-C/D'-D'-H-K-L

Y-Z-B-A-G-C-C/D-D
 Y-Z-B-A-G-C-C/D-H
 Y-Z-B-A-G-C-C/D-H-L
 Y-Z-B-A-G-C-C/D-H-K-L
 Y-Z-B-A-G-C-C/D-D'-H
 Y-Z-B-A-G-C-C/D-D'-H-L
 Y-Z-B-A-G-C-C/D-D'-H-K-L
 Y-Z-B-A-G-C-C/D'-D
 Y-Z-B-A-G-C-C/D'-H
 Y-Z-B-A-G-C-C/D'-H-L
 Y-Z-B-A-G-C-C/D'-H-K-L
 Y-Z-B-A-G-C-C/D'-D'-H
 Y-Z-B-A-G-C-C/D'-D'-H-L
 Y-Z-B-A-G-C-C/D'-D'-H-K-L
 Y-Z-B-A-G-C-C/D-C/D'-D
 Y-Z-B-A-G-C-C/D-C/D'-H
 Y-Z-B-A-G-C-C/D-C/D'-H-L
 Y-Z-B-A-G-C-C/D-C/D'-H-K-L
 Y-Z-B-A-G-C-C/D-C/D'-D'-H
 Y-Z-B-A-G-C-C/D-C/D'-D'-H-L
 Y-Z-B-A-G-C-C/D-C/D'-D'-H-K-L

952207-6709296

GGT/HYDROLYSIS SPLICING VARIANTS CONTINUED

E-B-A'

E-B-A-C-C/D-D
 E-B-A-C-C/D-H
 E-B-A-C-C/D-H-L
 E-B-A-C-C/D-H-X-L
 E-B-A-C-C/D-D'-H
 E-B-A-C-C/D-D'-H-L
 E-B-A-C-C/D-D'-H-X-L
 E-B-A-C-C/D'-D
 E-B-A-C-C/D'-H
 E-B-A-C-C/D'-H-L
 E-B-A-C-C/D'-H-X-L
 E-B-A-C-C/D'-D'-H
 E-B-A-C-C/D'-D'-H-L
 E-B-A-C-C/D'-D'-H-X-L
 E-B-A-C-C/D-C/D'-D
 E-B-A-C-C/D-C/D'-H
 E-B-A-C-C/D-C/D'-H-L
 E-B-A-C-C/D-C/D'-H-X-L
 E-B-A-C-C/D-C/D'-D'-H
 E-B-A-C-C/D-C/D'-D'-H-L
 E-B-A-C-C/D-C/D'-D'-H-X-L

E-B-A-G-C-C/D-D
 E-B-A-G-C-C/D-H
 E-B-A-G-C-C/D-H-L
 E-B-A-G-C-C/D-H-X-L
 E-B-A-G-C-C/D-D'-H
 E-B-A-G-C-C/D-D'-H-L
 E-B-A-G-C-C/D-D'-H-X-L
 E-B-A-G-C-C/D'-D
 E-B-A-G-C-C/D'-H
 E-B-A-G-C-C/D'-H-L
 E-B-A-G-C-C/D'-H-X-L
 E-B-A-G-C-C/D'-D'-H
 E-B-A-G-C-C/D'-D'-H-L
 E-B-A-G-C-C/D'-D'-H-X-L
 E-B-A-G-C-C/D-C/D'-D
 E-B-A-G-C-C/D-C/D'-H
 E-B-A-G-C-C/D-C/D'-H-L
 E-B-A-G-C-C/D-C/D'-H-X-L
 E-B-A-G-C-C/D-C/D'-D'-H
 E-B-A-G-C-C/D-C/D'-D'-H-L
 E-B-A-G-C-C/D-C/D'-D'-H-X-L

08736019-102296

EGFL1

AGCCATCTTCTCAAGTGTGCAGAGAGGAGAAAACCTTTCTGTGTCAATGGAGCCGAGTGC
S H L V K C A E K E K T P C V N G G E C
TTCATGCTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTGGCCAAATGAGTTT
P H V K D L S N P S R Y L C K C P N E P
ACTGCTGATCGCTGCCAAAACCTACGTAATGGCCAGCTTCTACAGTACGTCCTCACTCCCTTT
T G D R C Q N Y V H A S P Y S T S T P P
CTGTCTCTGCCTGAATAG
L S L P E *

(SEQ ID NO: 154)

FIGURE 38

06736019-102296
962207-6T09E290

03250151-1

(SDQ ID NO: 155)

FIGURE 39

207L3

AGCCATCTTGTCAAGTGTGCAGAGAGGAGAAAACTTTCTGTGTGAATGAGGCCGACTGC
S H L V K C A E K E K T F C V N G G E C
TTCATGCTGAAAGACCTTTCAAATCCCTCAAGATACTTGTGCAAGTGCCCAAATGACTTT
F H V K D L S N P S R Y L C K C P N E F
ACTGCTGATCCCTGCCAAACTACCTAATGCCAGCTTCTACAAAGCCGAGGAGCTCTAC
T G D R C Q N Y V H A S F Y K A E E L Y
TAA
.

(SEQ ID NO: 156)

FIGURE 40

08736019-102296
95220T-6T09E280

EGFLA

AGCCATCTTGTCAAGTGTGCAGAGAGGAGAAAACCTTTCTGTCTCAATCGAGGGCAGTGC
S H L V K C A E K E K T P C V N G G E C
TTCATGCTGAAAGACGTTTCAATCCCTCAAGATACTTGTCAAGTCCCCTCAATGAGTTT
P N V K D L S N P S R Y L C K C P N E P
ACTGCTGATCGCTGCCAAACTACGTAATGCCAGCTTCTACCAAGCATCTTGGGATTGAA
T G D R C Q N Y V N A S P Y K H L G I E
TTTATGGAGAAAGCGGAGGAGCTCTACTAA
P N E K A E E L Y •

(SEQ ID NO: 157)

FIGURE 41

06736019-102296

EGFLS

AGCCATCTTGTCAAAGTGTGCAGAGAACGAGAAAACTTTCTGTGTGAATGCGAGCGAGTGC
S H L V K C A E K E K T F C V N G G E C
TTCATGCTGAAAGACCTTTCAATCCCTCAAGATACTTGTGCAAGTGCACCTCGATTG
F H V K D L S N P S R Y L C K C Q P G F
ACTGCGAGCGAGATGTACTGAGAATGTGCCCATGAAAGTGCACCAAGCAAAAGTGCCTCA
T G A R C T E N V P H K V Q T Q E K C P
AATGAGTTTACTGCTGATCGCTGCCAAACTACGTAATGCCAGCTTGTACAGTACGTC
K E F T G D R C Q N Y V H A S P Y S T S
ACTCCCTTTCTGTGTGTGCTGCTGAATAG
T P F L S L P E *

(SEQ ID NO: 158)

FIGURE 42

08736019-102296

ZGFL6

AGCCATCTTCTCAAGTGTGCAGAGAAGGAGAAAACTTTCTGTGTGAATGGAGGCGAGTGC
S H L V K C A E K E K T P C V N G G E C
TTGATCGGTGAAAGACCTTTCAATCCCTCAAGATACTTGTGCAAGTCCCAACCTGGATTG
P H V K D L S N P S R Y L C K C Q P G F
ACTCGACCGAGATGTACTGAGAATGTGCCCATGAAAGTCCAAACCCAAAGAAAAGTCCCCA
T G A R C T E N V P H K V Q T Q E K C P
AATGAGTTTACTCGGTGATCGGTGCCAAACTACGTAATGCCAGCTTCTACAAAGCGGAG
H E F T G D R C Q N Y V H A S F Y K A E
GAGCTCTACTAA
E L Y *

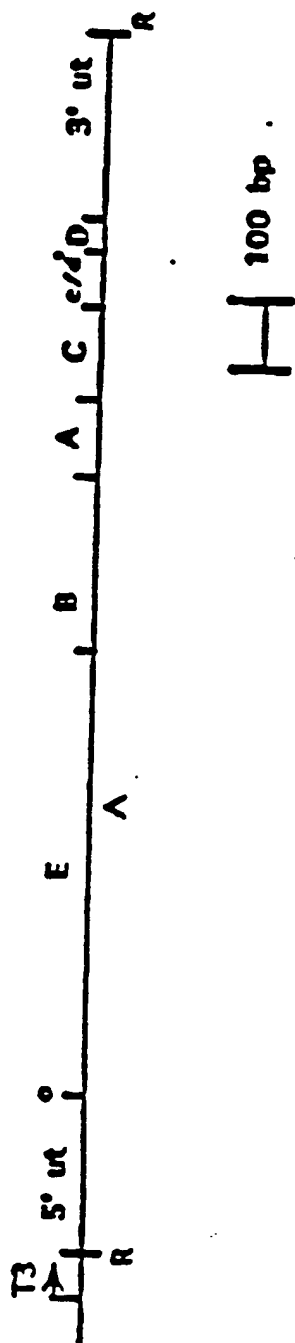
(SEQ ID NO: 159)

FIGURE 43

03736019-102296

FIGURE 44

GGF2HBS5



02-03-96

(SEQ ID NO: 167)

FIGURE 45 (1 of 3)

00736019-102296

780
E P Q E E A P Y L V K V E Q V W A V E A
K V E Q V W A A E
GCTII-1 & GCTII-11

840
G G L E X D S L L T V R L O T W G I P A
D L L L I V L G A W G P P A
GCTII-10 1 GCTII-3

900
P P S C Q R L E D S R Y I P P M E P D
P P V X Y Y I P P M E P E
GCTII-2

960
A M S T S R A P A A P R A S P P P L E T
A X S S G

1020
G R M L E X E V S R V L C E R C A L P P

1080
G L E E M X S Q E S A A G S E L V L R C
L V L R
GCTII-6

1140
E T S S E Y S S L R P X M P E N G E L

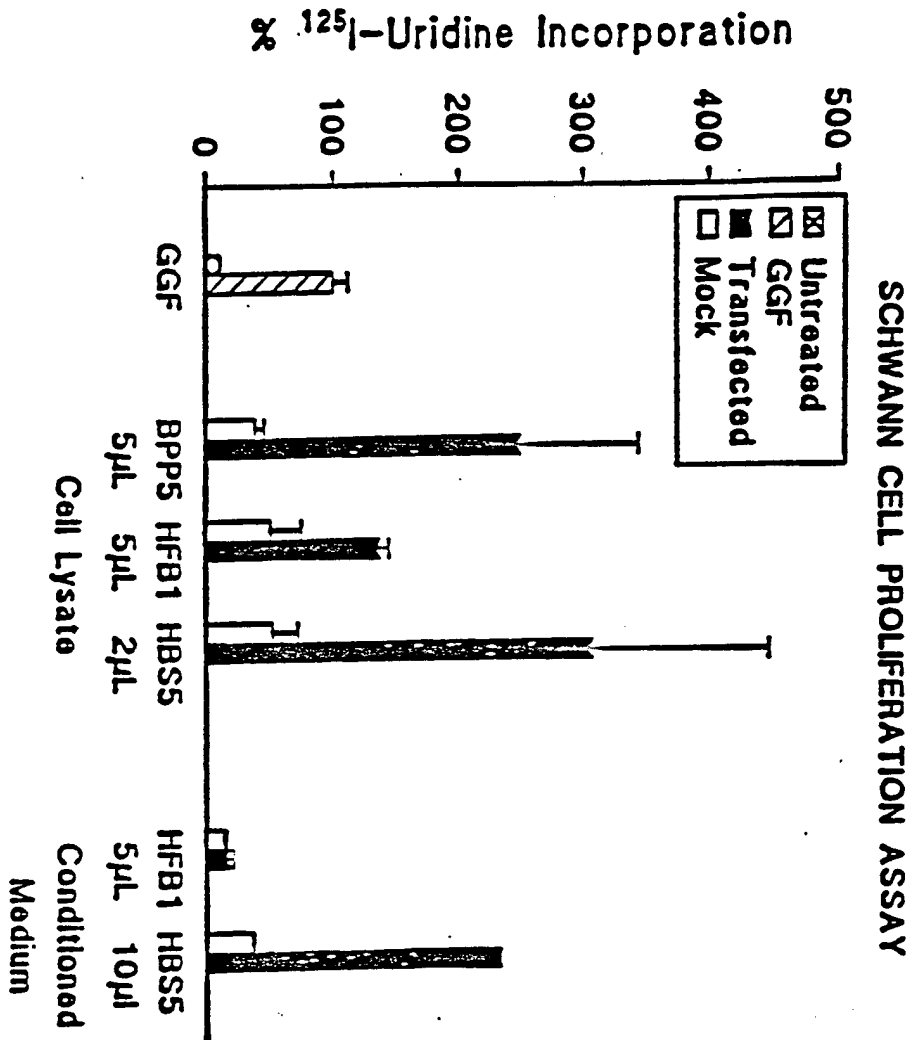
1200
M E E M X P Q N I X I Q E X P O E S E L

1260
E I N E A S L A D S G E Y M C E V I S X
K A S L A D S G E Y M X X
GCTII-12

1320
L O M D S A S A N I T I V E S N A T S T

FIGURE 45 (2 of 3)

FIGURE 46



08736019.102296

FIGURE 47

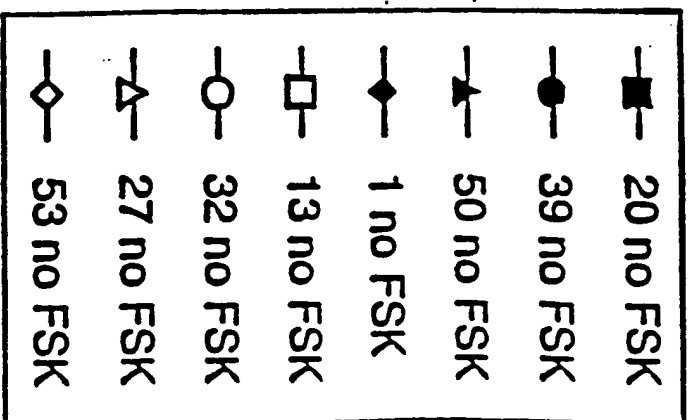
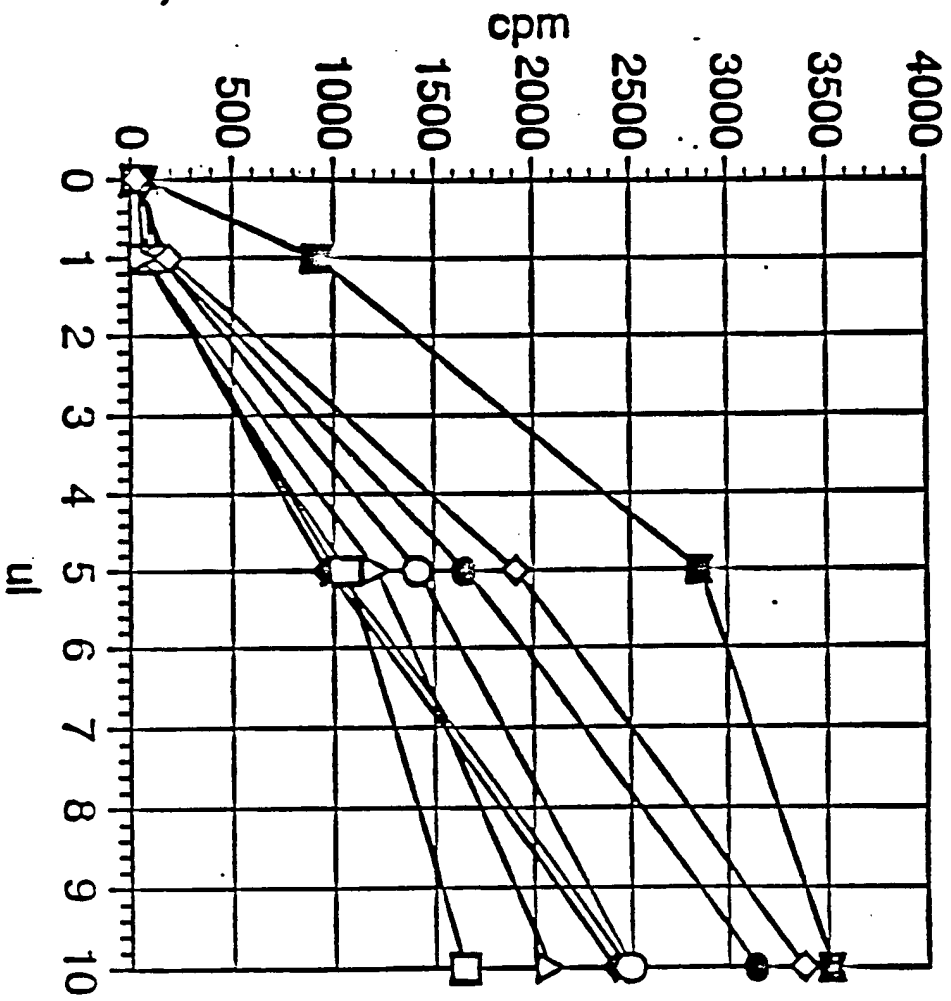


FIGURE 48

Schwann Cell Assay/Baculovirus Clones

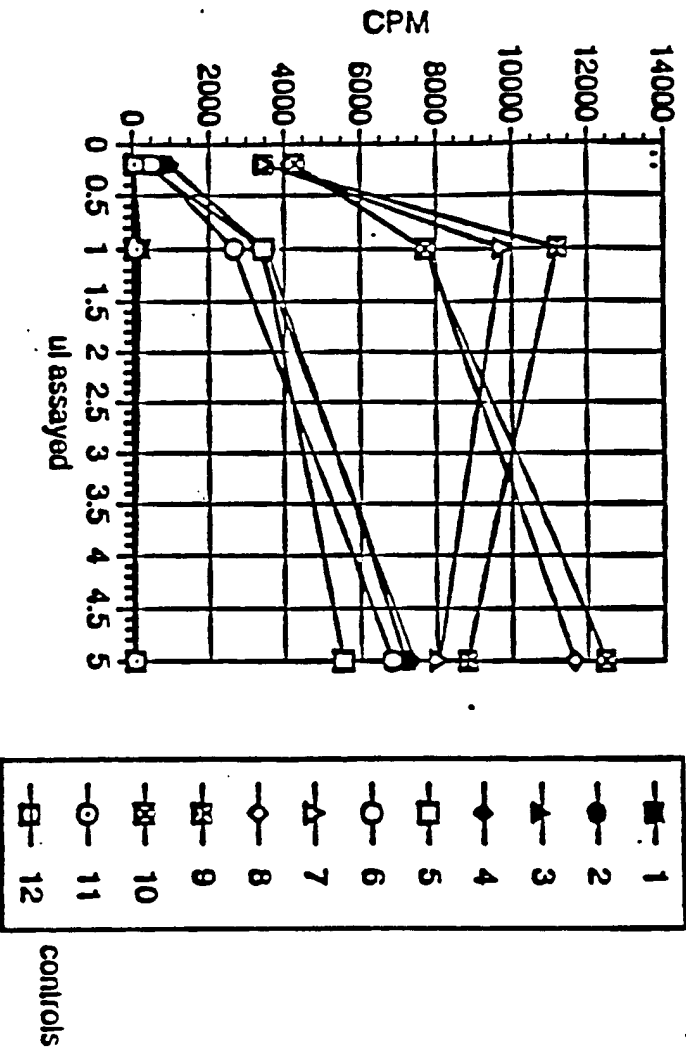
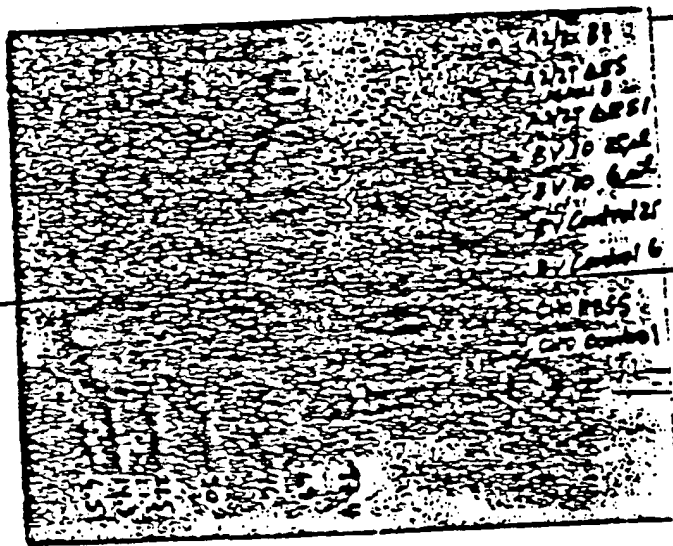
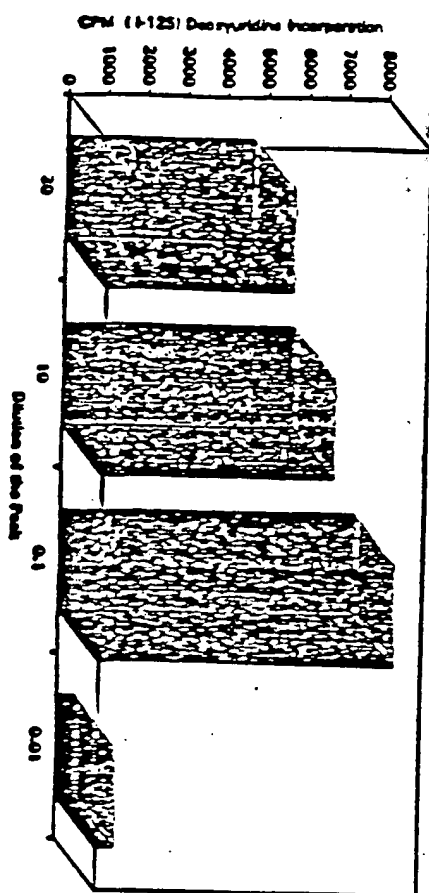


FIGURE 49



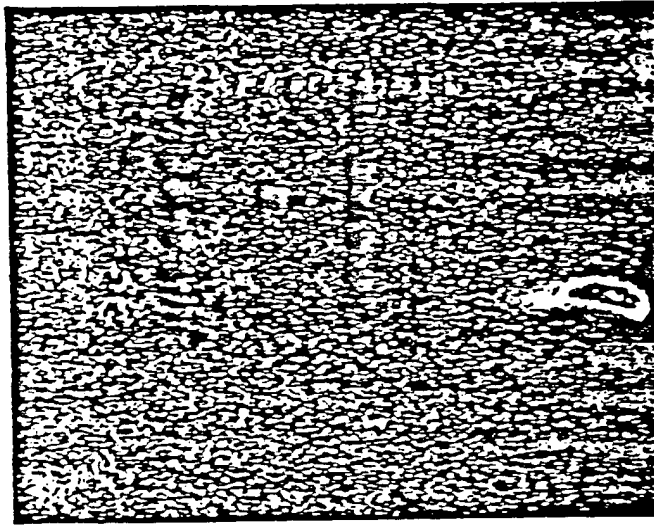
08736019.102296

FIGURE 50A



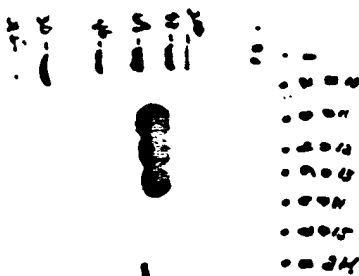
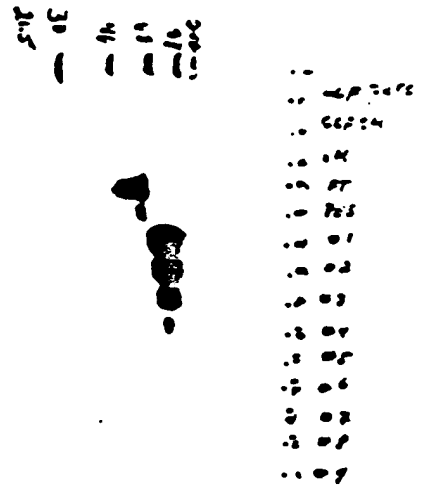
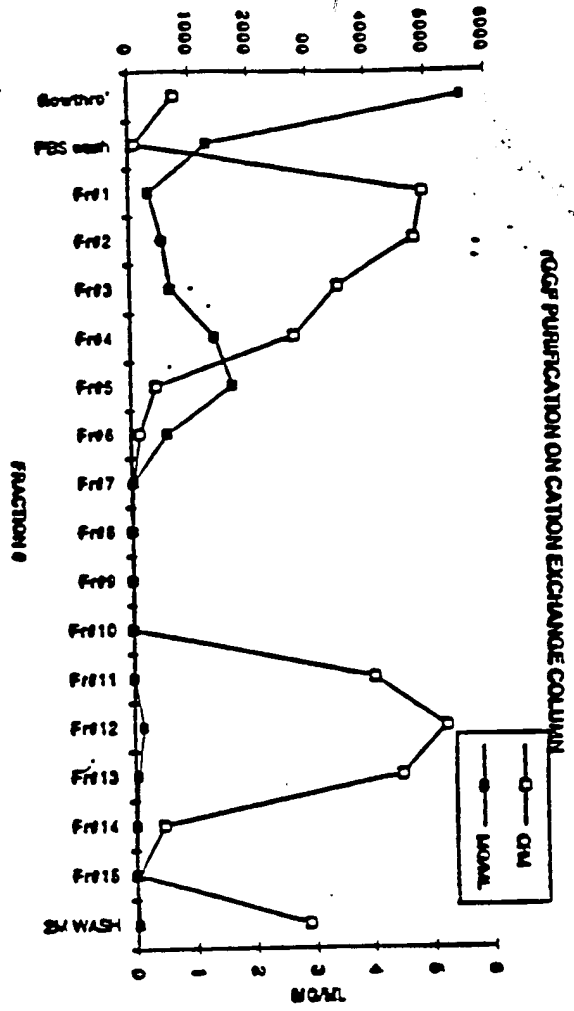
08736019.102296

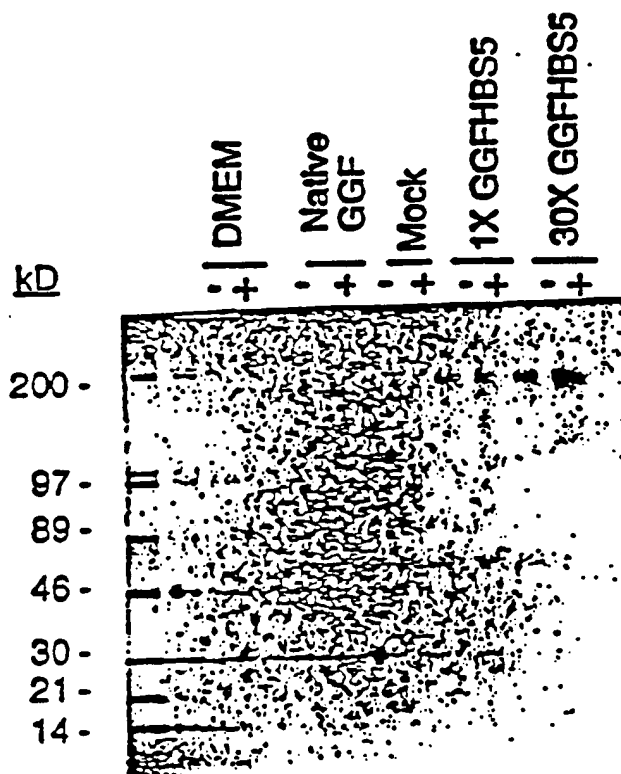
FIGURE 50B



08736019 102296

FIGURE 51





062301910000

DISORDERED SEQUENCES OF HUMAN AND MONKEY OXIAL GROWTH FACTORS

1

SEQ ID NO: 170
COPIESS 1
WVWUUA PRRACH FQPVQA QRPQGA AARBSPPPL PLPL L L L TTAALA PQAAANONTPA PQAGS

11-9 . 11-1

61 VCTESPPEVQSVQELAQRAVVVDRKKVHPQRIRQQALDRKAAANJQWQANQOQDHRPPAA

II-1

121 0PRL0PPAEKPI LLAUZZTVDSPTA PVPBAGHPF0EEAPFLVKVHQVAVAKOOLJ0JDSL
II-3 II-2

101 LTVRLQWHPAPPSCONLRQSGRYIPTHETPDANSTGRAPAAFTQSPPLATONMLKUEV

3

COPIES 241	BRVLCRC.....	ALPPLKRGDEANOSI
COPIES 1	O CHSKROROKOKROROSORFLBANDSEP	
COPIES 1	R R O D VP OF R V	

SEQ	ID NO:	171
SEQ	ID NO:	172

III-14
III-11 1-7, 11-12,
III-13
III-6
III-10

LVLACET96SKYSELAF70P70NOMELANRUKPWQIQRPOKSHALINRUASLAD80ETMC

11-13 3

220	KVIERLONDSASNUITVERH.....ADSTB	
113	ELTONPAETMOAYVESBPRIEVESTOANTSGB	T T T
113		

9 51-11 8

354 TTOTSHLVKCAERKPTFCVNOGCEPMVKDLSNPSHLYLCECPNEPTDRCQNTVNSFTBT
173
173
173 A

9

084757465

232 232 232

Fig. 53

7360/9

FIG. 5A

